STIC-Biotech/ChemLib



64186

From: Sent: To: Subject: Hunt, Jennifer Wednesday, April 10, 2002 10:12 AM STIC-Biotech/ChemLib Seq Search for 09/234,208

Please search and interference search SEQ ID NO:1 and 2 of 09/234,208.

Thanks,

Jennifer Hunt Patent Examiner, Art Unit 1642 CM1-8D06 (mailbox 8E12) (703)308-7548

> Point of Contact: Toby Port Technical Info. Specialist CM1 6A04 703-308-3534

RECEIVED

Searcher:
Phone:
Location:
Date Picked Up: 4/11
Date Completed: 4/12
Searcher Prep/Review: 1/0
Clerical:
Online time: //

TYPE OF SEARCH:
NA Sequences:
AA Sequences: 2
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
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VENDOR/COST(where applic.)
STN:
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Human semaphorin z
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Human PR04353 poly
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ALIGNMENTS

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AAY97241 standard; Protein;

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HER-2; erbB-2; oncogene; receptor-like tyrosine kinase; insertion; extracellular domain IIIa; antagonist; intron 8; C-terminal extension; truncated HER-2; p68; dimerization inhibitor; cytostatic. WPI; 2000-499287/44. N-PSDB; AAA53783. HER-2 C-terminal extracellular domain IIIa Doherty JK, 20-JAN-1999; 03-AUG-2000 WO200044403-A1 Homo sapiens. 04-DEC-2000 (UYOR-) UNIV OREGON HEALTH SCI. 20-JAN-2000; 2000WO-US01484 Clinton GM, Adelman JP; (first entry) 9905-0234208

Using polypeptides and antibodies that bind to the extracellular domain of the receptor-like tyrosine kinase HER-2 to treat solid tumors of the breast, lung, ovaries and colon

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           carcinoma cells in culture and is found in serum of some cancer patients and may be a serum marker of metastatic breast cancer. An alternative HER-2 mRNA of 4.8 kb with a 274 bp insert (intron 8) has been identified. The retained intron is in-frame and encodes a 79 amino acid extension designated ECDIIIa (the present sequence), which is inserted at residue 340 of pla85-HER-2. The alternative mRNA predicts a truncated HER-2 protein (approximately 68 kDa) that lacks the transmembrane and
Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and may be a serum marker of metastatic breast cancer. An alt HER-2 mRNA of 4.8~\rm kb with a 274~\rm bp insert (intron 8) has been identified. The retained intron is in-frame and encodes a 79~\rm kc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HER-2/neu (erbB-2) oncogene encodes a receptor-like tyrosine kinase. extracellular domain of p185-HER-2 is proteolytically shed from brea extracellular domain of p185-HER-2 is proteolytically shed from brea extracellular domain of culture and is found in serum of some cancer path
                                                                                        04-DEC-2000
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Pred. No. 8.2e-32;
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HER-2; erbB-2; oncogene; receptor-like tyrosine kinase; insertion; extracellular domain IIIa; antagonist; intron 8; C-terminal extens truncated HER-2; p68; dimerization inhibitor; cytostatic.

extension;

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Truncated HER-2, p68-HER-2

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HER-2/neu (erbB-2) oncogene encodes a receptor-like tyrosine kinase. The extracellular domain of p185-HER-2 is proteolytically shed from breast carcinoma cells in culture and is found in serum of some cancer patients and may be a serum marker of metastatic breast cancer. An alternative identified. The retained intron is in-frame and encodes a 79 amino acid extension designated ECDIIIa (the present sequence), which is inserted at residue 340 of p185-HER-2. The alternative mRNA predicts a truncated HER-2 protein (approximately 68 kDa) that lacks the transmembrane and intracellular domains (see AAY97240). p68HER-2 specifically binds to p185-HER-2 without activating HER-2. It could therefore block of imerization of p185-HER-2. The p68HER-2 polypeptide binds to a site on the ECD of HER-2 that is different from the site of binding for
                                                  Herceptin (RTM) (a marketed humanized monoclonal antibody that is used for the treatment of cancer and binds to the ECD of HER-2). The methods compositions, polypeptides and antibodies are used to treat solid tumours such as breast cancer, small cell lung carcinoma, ovarian cancer.
                                                                                                                                                                                                                                                                                                Claim
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                                                                                                                                                                                                                                                                                                                                   ing polypeptides and antibodies that bind to the extracellular the receptor-like tyrosine kinase HER-2 to treat solid tumors
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Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                             The invention provides a method for detecting a US (sub)type hepatitis E virus (US-HEV), or its naturally occurring variants in a sample by treatment with a binding partner specific for a marker of the virus, and then detecting any complex formed. The method is used to diagnose infection with US-HEV. Polypeptides from US-HEV, antibodies specific for open reading frames (ORF) in US-HEV and host cells expressing these ORFs are useful in vaccines or for passive immunisation. The polypeptides are also used to raise specific antibodies (useful as immunoassay reagents). Fragments of nucleic acid from US-HEV are useful as primers and probes in usual hybridisation and amplification assays for detecting infection.
                                                                                                                                                                                                                                                                                                                                                            Sequence
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Matches 27
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central nerve regeneration promoter
                           Semaphorin Z; central nerve extension; rat;
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                                                                                                                                                                                                                                               AAW19857 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ragments of nucleic acid from US-HEV are useful as primers and prob-
usual hybridisation and amplification assays for detecting infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                     entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 86; DB 20;
Pred. No. 0.19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Secreted protein; transmembrane protein; pro1484; pro4334; Pro
pro1889; pro1890; pro1887; pro1785; pro4353; pro4357; pro4405;
pro4352; pro4380; pro4354; pro4408; pro5737; pro4425; pro5990;
pro4424; pro4422; pro4430; pro4499; tumour; obesity; diabetes;
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06-DEC-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                action which can be used as promoters of central nerve regeneration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   insulinemia; kidney disorder; Bergers disease; nephropathy;
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95JP-0345187.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "N-myristoylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "N-glycosylation site"
                                                                                                                                                                                                                                                          "N-myristoylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cGMP-dependent
                                                                                                                                                                                                                                           site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein kinase
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                                                                                                                                RESULT
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WO200056889-A2

AAU12443 ID AAU1

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rapeqppapge-ptpdgrl SVPISPVSVGRGPDPDAHV

70

gphdldsgllptpeqtplpqkrlptp-hphphalgprawdhghpllpasasssllllapa 756 GTH----SLLPRPAAVPVPLRMQPGPAHPVLSFLRP-SWD----LVSAFYSLPLAPLSPT

Conservative

33;

Indels

11;

Gaps 51

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AAU12443 standard; Protein;

888 ₿

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CC The present sequence represents a secreted or transmembrane polypeptide. CC The specification describes polypeptides designated PRO1484, PRO4334, CC PRO1322, PRO1889, PRO1887, PRO1887, PRO4785, PRO43537, PRO4357, PRO4405, CC PRO4356, PRO4352, PRO4380, PRO4354, PRO4408, PRO5737, PRO4425, PRO5990, CC PRO6030, PRO4424, PRO4422, PRO4430 and PRO4499, PRO1889 polypeptide is CC useful for diagnosing tumour in a mammal. The polypeptides, their CC agonists and antagonists are useful treating a condition associated with CC expression or activity of the polypeptide. Conditions treated include CC obssity, diabetes or hyper-or hypo-insulinemia. The polypeptides are CC capable of inducing proliferation of mammalian kidney mesangial cells cand are therefore useful for treating kidney disorders associated with CC and are therefore useful function such as Bergers disease or other CC nephropathies associated with Schonlein-Henoch purpura, celiac disease, CC decrmatitis herpetiformis or Crohns disease. The nucleic acids may be used to generate transgenic animals for use in development and screening of CC therapeutically useful reagents and also for chromosome identification and conditions and the conditions
   Query Match
Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-1999
24-MAR-1999
31-MAR-1999
05-APR-1999
27-APR-1999
27-APR-1999
27-APR-1999
27-APR-1999
04-MAY-1999
04-MAY-1999
04-MAY-1999
08-JUN-1999
08-JUN-1999
08-JUN-1999
03-AUG-1999
                                                                                                                                                                                                                                      to generate transgenic therapeutically useful and tissue typing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tumour in a mammal, polypeptide and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Desnoyers L,
Stewart TA,
                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12; Fig 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel secreted and transmembrane polypeptides useful for diagnosing tumour in a mammal, for identifying agonists and antagonists of the polypeptide and for therapeutic use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
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990S-0132371
990S-0132379
990S-0132379
990S-0132375
990S-0131750
990S-0146790
990S-0146670
990S-0146670
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                                     20.0%;
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Score 83.5; D
Pred. No. 0.76
7; Mismatches
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Zhang Z;
                                     DB
.76;
                                                                 Length
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11-FEB-2000;
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24-FEB-2000;
24-FEB-2000;
01-MAR-2000;
20-MAR-2000;
21-MAR-2000;
30-MAR-2000;
17-MAY-2000;
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20-DEC-1999;
20-DEC-1999;
30-DEC-1999;
30-DEC-1999;
06-JAN-2000;
06-JAN-2000;
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01-DEC-1999;
02-DEC-1999;
02-DEC-1999;
02-DEC-1999;
09-DEC-1999;
          AAU12172-AAU12446 represent novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bloactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of
                                                                                                                                               Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical
                                                                                                                          Claim 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cartilage; ear; proliferation; glucose; free fat
adipocyte; A-peptide; factor VIIA; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human secretory and transmembrane;
breast; prostate; cervical; tumour
                                                                                                                                                                                                                                                               Gerritsen
                                                                                                                                                                                                                                                                           Baker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200140466-A2
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DB; AAS21515.
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 necrosis
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ME, Goddard
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2000WO-US00376
2000WO-US03565
2000WO-US04341
2000WO-US04414
2000WO-US04914
2000WO-US04914
2000WO-US05601
2000WO-US05601
2000WO-US07377
2000WO-US07532
2000WO-US014042
2000WO-US14042
2000WO-US14941
2000WO-US14941
2000WO-US3087373
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                                                                                                                          544;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US28301
99WO-US28634
99WO-US28551
99WO-US28564
99WO-US28565
99WO-US28565
99WO-US30095
99WO-US30911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US30999.
99WO-US31243.
factor-alpha (TNF-alpha) from human blood,
                                                                                                                        813pp;
                                                                                                                                                                                                                                                Deforge L, Desnoyers L,
A, Godowski PJ, Gurney J
Tumas D, Watanabe CK, W
                                                                                                                         English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRO; mammalian; cancer; lung;
necrosis factor-alpha; TNF-alpha;
cose; free fatty acid; skeletal muscle;
                                                                                                                                                                                                                                                L, Filvaroff E, ey AL, Sherwood S Wood WI, Zhang
                                                                                                                                                                                                                                             1 S;
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AAY31402
ID AAY3
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis vaccine; p
                                                                                                                                                                 Detection of United States isolates of hepatitis
                                                                                                                                                                                                                           Dawson
                                                                                                                                                                                                                                                                                                                                              W09919732-A1
                                                                                                                                                                                                                                                                                                                                                                                                                             HEV US and CMP-KDO synthetase (CKS) fusion protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY31402 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                 (ABBO ) ABBOTT
                                                                                                                                                                                                                                                                          15-OCT-1997;
                                                                                                                                                                                                                                                                                                15-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                    Hepatitis E virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-OCT-1999
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                                                                                                                                                                                        1999-288017/24
DB; AAZ00278.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVPISPVSVGRGPDPDAHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gphdldsgllptpeqtplpqkrlptp-hphphalgprawdhghpllpasasssllllapa 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTH----SLLPRPAAVPVPLRMQPGPAHPVLSFLRP-SWD----LVSAFYSLPLAPLSPT 51
                                                                                                                                                                                                                           GJ,
                                                                                                                                                                                                                                                                                                                                                                                            passive
                                                                                                                                                                                                                                                                                                                                                                                                        Œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    888 AA;
                                                                                                                                                                                                                           Desai SM,
                                                                                                                                                                                                                                                                                                                                                                                                        virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                          97US-0061199
                                                                                                                                                                                                                                                                                                98WO-US21941
                                                                                                                                                                                                                                                                                                                                                                                              immunisation
                                                                                                                                                                                                                                                                                                                                                                                                      HEV; binding partner; virus; US-HEV infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein; 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.0%;
                                                                                                                                                                                                                           Erker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 83.5;
Pred. No. 0.
                                                                                                                                                                                                                           JC,
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                                                                                                                                                                                                                           Mushahwar
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                                                                                                                                                                 E virus
                                                                                                                                                                                                                           Schlauder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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The invention provides a method for detecting a US (sub)type hepatitis E virus (US-HEV), or its naturally occurring variants in a sample by treatment with a binding partner specific for a marker of the virus, and then detecting any complex formed. The method is used to diagnose infection with US-HEV. Polypeptides from US-HEV, antibodies specific for open reading frames (ORF) in US-HEV and host cells expressing these ORFs are useful in vaccines or for passive immunisation. The polypeptides are also used to raise specific antibodies (useful as immunoassay reagents). Fragments of nucleic acid from US-HEV are useful as primers and probes in usual hybridisation and amplification assays for detecting infection.

Example 10;

Page _240;

260pp; English.

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AAY31403
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Matches 23
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Best Local
                                                                                                                The invention provides a method for detecting a US (sub)type hepatitis E virus (US-HEV), or its naturally occurring variants in a sample by treatment with a binding partner specific for a marker of the virus, and then detecting any complex formed. The method is used to diagnose infection with US-HEV. Polypeptides from US-HEV, antibodies specific for open reading frames (ORF) in US-HEV and host cells expressing these ORFs are useful in vaccines or for passive immunisation. The polypeptides are also used to raise specific antibodies (useful as immunoassay reagents). Fragments of nucleic acid from US-HEV are useful as primers and probes in
                                                                                                                                                                                                                                                                                                              15-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .Sequence
                                                                                                         Fragments of nucleic acid from US-HEV are useful as primers and probeusual hybridisation and amplification assays for detecting infection.
                                                                                                                                                                                                  Example 10; Page 241; 260pp; English.
                                                                                                                                                                                                                                             WPI; 1999-288017/24
                                                                                                                                                                                                                                                              Dawson
                                                                                                                                                                                                                                                                                                                                                                Hepatitis E virus
                                                                                                                                                                                                                                                                                                                                                                                                          HEV US
                                                                                                                                                                                                                                                                                                                                                                                                                          12-OCT-1999
                                                                                         Sequence
                                                                                                                                                                                                                                                                                               15-OCT-1997;
                                                                                                                                                                                                                                                                                                                                 22-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis E virus; HEV; binding partner; virus; US-HEV infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY31403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY31403 standard;
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                57
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88
                                                         Local Similarity
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V 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gvtglilsps--pspifiqptps-ppmsfhnpglelaldsrpaplaplgvtspsapplpp 113
              gvtglilsps--pspifiqptps-ppmsfhnpglelaldsrpaplaplgvtspsapplpp 113
                              GTHSLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPL---SPTSVPISP 57
                                                                                                                                                                                                                                                              GJ, Desai SM,
                                                                                                                                                                                                                                                                                                                                                                                                         recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity 37.7
23; Conservative
                                                                                                                                                                                                                                                                              ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                 passive immunisation
                                                                                                                                                                                                                    of United States isolates
                                                                                          132 AA;
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                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                                                                                        protein plorf2-2.
                                                       19.6%;
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                                                                                                                                                                                                                                                              Erker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 82;
Pred. No.
                                                         Score 82;
Pred. No.
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                                                Mismatches
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                                                        0.12;
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                                                                20;
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                                                 22;
                                                               Length 132;
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                                                                                                                                                                                           This sequence represents a neurocan polypeptide. This protein has several biological activities, including cell adhesion, leukocyte-endothelial cell recognition, tissue-related inflammation allergies, cellular and/or humoural hypersensitivity, trauma, neuronal development, and cell transport and/or infection. Compositions containing them can be used as modulators of these conditions, and may be used as therapeutic, diagnostic, and/or research tools. Neurocan peptides can be used to mimic proteins, such as lectins, cell adhesion molecules, versicans, aggrecans or gelsolins, as receptor or effector subtypes. The protein can be used to treat diseases involving a qualitative or quantitative pathological abnormality of cell adhesion or leukocyte-endothelial cell recognition, or a functional masses and or leukocyte-endothelial cell recognition.
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                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotic neurocan polypeptide(s) with epidermal growth factor, lectin or complement binding activity - used in the diagnosis, treatment or research of hypersensitivity and allergic diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAQ57710.
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                                                                                                                                              Sequence
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 SVP----ISPVSVGRGPDPD 67
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                                                                                                                                                                      lipid, carbohydrate, saccharide, nucleoside,
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                                                                                                                                                                                                                                                                                                                                                                  virus (US-HEV), or its naturally occurring variants in a sample by treatment with a binding partner specific for a marker of the virus, and then detecting any complex formed. The method is used to diagnose infection with US-HEV. Polypeptides from US-HEV, antibodies specific for open reading frames (ORF) in US-HEV and host cells expressing these ORFs are useful in vaccines or for passive immunisation. The polypeptides are also used to raise specific antibodies (useful as immunoassay reagents). Fragments of nucleic acid from US-HEV are useful as primers and probes in usual hybridisation and amplification assays for detecting infection. The present sequence represents a HEV-US2 ORF3 protein.
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36.1%;
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                                                                                                                                                                                                                       78;
No.
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                                                                                                                                                                                                                     DB 20;
0.31;
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RESULT 13 AAW31852

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RESULT 14
AAW93407
ID AAW934
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AC AAW934
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                                                                                                                                                                                                                                                                                                                                                                                         This novel 74 kDa protein is encoded by an open reading frame of a Mycobacterium tuberulosis DNA fragment (see AAT93610) containing polymorphic GC-rich sequences. Its amino acid sequence shows a high proline content, but there is no homology to any known proline-rich antigens of mycobacteria. Novel M. tuberculosis proteins (see AAM91851-57) are claimed. These can be produced as recombinant proteins, especially in bacterial, yeast, fungal or higher eukaryote host cells, and used for diagnosing tuberculosis and other mycobacterial infections in humans or animals. The claimed proteins can also be used for epidemiological studies, for monitoring vaccination, and for the development of vaccines and
                Swine HEV ORF 3 protein
                                                                                                                                                                                                                                                                                                                                                                                  anti-mycobacterial drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New DNA and related proteins or RNA derived from M. tuberculosis used for diagnosis of mycobacterial infections, monitoring vaccination and development of anti-mycobacterial agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antimycobacterial; antibiotic;
                                                                       AAW93407;
                                                                                                AAW93407 standard; Protein; 122 AA
                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-549750/50.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-APR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tuberculosis; mycobacteria; infection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis 74 kDa protein
                                         11-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GBFB ) GBF GES BIOTECH FORSCHUNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW31852 standard;
                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                     69
                                                                                                                                                                                                60 VGRGPDPDA 68
                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                     4 SLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSP----TSVPISPVS 59
                                                                                                                                                                                                                          alaplppappapaepkskppfppappappcwmlvsaappcppappappkpkskapfppvp 68
                                                                                                                                                                   -pappa 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fig 13; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                         763 AA;
                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Honisch C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein; 763 AA
                                                                                                                                                                                                                                                                                               18.7%;
34.8%;
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                                                                                                                                                                                                                                                                                  4.
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Pred. No. 2.
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                                                                                                                                                                                                                                                                                               DB 18; Length 763; 2.5;
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                                                                                                                                                                                                                                                                                 Gaps
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Human; primer;

detection; diagnosis; antisense therapy; gene therapy

Human protein sequence SEQ ID NO:13931.

AAB93933; 26-JUN-2001

(first entry)

AAB93933 standard; Protein; 329

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07-FEB-2001

EP1074617-A2

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RESULT 15
AAB93933
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Best Local :
                                                                                                                                                                                                                                                                                                                                                   can be used in vaccines for immunising against HEV infection. The swine HEV can be used in humans to prevent possible infection by human HEV. The swine HEV can also be used as a therapeutic treatment for infection by other strains of HEV. The swine HEV can also be used for the production of antibodies which can be used in therapy, detection and diagnosis. The products can also be used for determining the susceptibility of cells or organs to infection with swine HEV. The swine HEV is particularly useful for the development of agents for the prevention, treatment and detection of human HEV because it is not a human virus and thus can be handled both experimentally and clinically without fear of severe infection and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a swine hepatitis E virus (HEV) and its natural mutants which are capable of cross-reacting with antibodies reactive with a human HEV strain or natural mutants. The HEV and the proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Swine hepatitis E virus; HEV; cross-reaction; antibody; human; therapy; vaccine; immunise; infection; detection; diagnosis; prevention.
                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated swine hepatitis E virus - used to develop products for the diagnosis, prevention and treatment of hepatitis E virus infection in mammals, particularly humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-132270/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Fig 3B; 70pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Emerson SU,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis E virus:
                                                                                                                                                                                                                                                                                                                                        contamination.
                                                                      112 v 112
                                                                                                                                                                                                              Local Similarity 36.1 hes 22; Conservative
                                                                                                       58 V
                                                                                                                                          55
                                                                                                                                                                           1 GTHSLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPL---SPTSVPISP 57
                                                                                                                                        gvtglilsps--pspifiqptpslp-msfhnpglefaldsrpaplaplgvtspsapplpp 111
                                                                                                         58
                                                                                                                                                                                                                                                                                                     122 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98WO-US14665
                                                                                                                                                                                                                               18.4%; Score 77; 36.1%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Purcell RH;
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                                                                                                                                                                                                                                0.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        to the 5602 nucleotide sequences defined in the specification, where the complementary strand of a polynucleotide which comprises one of colligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide complementary to the complementary strand of a polynucleotide which comprises a 5'-end complementary to a complementary to a colligonucleotide comprises a 3'-end sequence complementary to a colligonucleotide which comprises a 3'-end sequence complementary to a colligonucleotide comprises a 3'-end sequence, where the colligonucleotide comprises at least 15 nucleotides and the combination of colligonucleotide comprises at selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in colligonucleotide comprises are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are useful for synthesising polynucleotides, collection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs casaily without any specialised methods. AAH33630 to AAH33630 and COL AAH36331 to AAH38742 represent human amino acid sequences; and AAH3629 to AAH3632 conference inventors.
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JUL-1999; 99JP-0248036.
27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; SEQ ID 13931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ota T,
                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                        of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ishii S,
                                                                                                     277 aslsfntpey 286
                                                                                                                                                                                     68 AHVAVNLSRY 77
                                                                                                                                                                                                             8 RPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSVGRGPDPD 67
                                                                                                                                                                                                                                                                             24;
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                                                                                                                                                                                                                                                                                                                                                                                   329 AA;
                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                               18.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2537pp + CD ROM; English
                                                                                                                                                                                                                                                                         Score 77; DB 22; Pred. No. 1.2; 8; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saito K, Yo
K, Otsuki T;
                                                                                                                                                                                                                                                                             24;
                                                                                                                                                                                                                                                                                                                   Length 329;
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Maximum Match 100%
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1: pir1:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	œ	7	0	ر.	4	ω	2	1	Result No.
70	70	70	70	70	70.5	70.5	70.5	70.5	71	71.5	72	72	72.5	73	74.5	75	75	76	76	76.5	77	77.5	78	80	80	81	81	81.5	Score
16.7	16.7	16.7	6	16.7	16.9		16.9	16.9	17.0	17.1	17.2	17.2	17.3	17.5	17.8	17.9	17.9	18.2	18.2	18.3	18.4	18.5	18.7	19.1	19.1	19.4	19.4	19.5	Query Match
2318	2187	954	650	491	1268	788	443	291	906	2441	1914	440	518	1520	894	1952	189	848	356	1110	503	217	249	1840	1834	1006	200	1257	Length
N	N	N	N	N	N	-	ν	N	2	N	N	N	2	2	N	ν	N	N	N	N	2	N	N	Ŋ	_	N	N	N	DB
\$45306	T30826	E86174	S14181	S14182	S52781	JDVLHH	T27877	S27721	A71438	S39161	T42635	A44081	F70831	T00273	T13029	T48814	D49600	S48273	A96826	T19673	T19319	T51031	S72619	G85422	JDMU1	G86292	H84715	S28764	ID
notch 3 protein -	nascent polypeptid	protein F19P19.26	RNA	DNA-directed RNA p	ouse	_		hypothetical prote	probable resistanc	in	tenascin Y precurs	e op	probable PPE prote			hypothetical prote	genome-linked prot		_		hypothetical prote	μ.	_	hypothetical prote	_	hypothetical prote	probable phytocyan	neurocan precursor	Description

ALIGNMENTS

C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 01-Sep-1995 #text_change 04-Feb-2000

R;Rauch, U.; Karthikeyan, L.; Maurel, P.; Margolis, R.U.; Margolis, R.K. J. Biol. Chem. 267, 19536-19547, 1992

C; Accession:

neurocan precursor - rat

A; Cross-references: EMBL.M97161; NID:g205649; PIDN:AAC37679.1; PID:g205650
A; Cross-references: EMBL.M97161; NID:g205649; Complement factor H repeat homology;
C; Superfamily: aggrecan; C-type lectin homology; Complement factor H repeat homology;
C; Keywords: chondroitin sulfate proteoglycan; glycoprotein
F; 1-22/Domain: signal sequence #status predicted <SIG>F; 23-1257/Product: neurocan #status predicted <MAT>F; 23-1257/Product: neurocan #status predicted <MAT>F; 274-355/Domain: link protein repeat homology <LNK2>F; 274-355/Domain: link protein repeat homology <LNK2>F; 364-366/Region: cell attachment (R-G-D) motif
F; 93-984/Domain: EGF homology <EGF>F; 1029-1149/Domain: C-type lectin homology <LCH>F; 1156-1212/Domain: C-type lectin homology <LPD>F; 1156-1212/Domain: complement factor H repeat homology <FHD>F; 1156-1212/Domain: complement factor H repeat homology <FHD>F; 1156-1212/Domain: site: chondroitin sulfate (Ser) (covalent) #status predicted F; 372,410/Binding site: chondroitin sulfate (Ser) (covalent) #status experimental C;Accession: H84715
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999 probable phytocyanin [imported] - Arabidopsis thaliana
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 RESULT H84715 Ş 밁 δÃ DЬ A; Title: Cloning and primary structure of neurocan, a developmentally regulated, A; Reference number: S28764; MUID:92406907
A; Accession: S28764 A; Molecule type: mRNA A; Residues: 1-1257 < RAU> Query Match Best Local Similarity Matches 670 SVPEEQAVRPVSFG-AEDPE 688 610 SSIPSEALSAVSLQASPGDGSPDFPIVAMLRAPKLWLLPHSTLVPNVSPIPLSPASPLPS 669 52 SVP----ISPVSVGRGPDPD 67 4 SLLPRPAAVPVPLRMQPG---PAHPVLSFLR-----PSWDLVSAFYSLPLAPLS--PT 51 Conservative 19.5%; Score 81.5; DI 35.0%; Pred. No. 2.7; 10; Mismatches DB 25; 2: Length 1257; Indels 17; Gaps ر.

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A;Title: Sequence and and A;Referrence number: A844'A A;Referrence number: A84715 A;Accession: H84715 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-200 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Genetics:
A; Map posit
             DNA-directed RNA polymerase (EC 2.7.7.6) II largest chain - Arabidopsis thal N;Alternate names: DNA-directed RNA polymerase II 205K chain; protein F4B14. C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 31-Mar-1993 #sequence_revision II-Jun-1999 #text_change 20-Aug-1999 C;Accession: T04690; S12071; S27346; S11960 R;Bevan, M; Rose, M.; Hempel, S.; Entian, K.D.; Hohelsel, J.; Mewes, H.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mail Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; & ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis A; Reference number: A86141; MUID:21016719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein AAF82153.1 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: G86292
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A;Map position: 2
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A; Residues: 1-1006 <
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A; Accession: G86292
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n, L.;
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Liu, S.X.; Liu, Z.A.; Luros, J.S.;
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No.
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K.D.; Hoheisel,
October 1998
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                 J.; Mewes, H.W.; Mayer,
                                                                                        Arabidopsis thaliana; protein F4B14.70
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Maiti, R.; Ma
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war, K.
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               A;Cross-references: GB:NC_001268;
C;Genetics:
A;Gene: AT4935800
A;Map position: 4
C;Superfamily: human DNA-directed
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A; Residues: 1-1840 <
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                                                                                                                                                                                       A; Title: Sequence and analysis of chromosome A; Reference number: A85001; MUID: 20083488
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NID: g7270532;

PIDN:CAB81489.1;

GSPDB:GN00140

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C;Superfamily: human DNA-directed RNA polymerase II largest chain C;Keywords: DNA binding; nucleotidyltransferase; phosphoprotein; F;66-109/Region: zinc finger CCCC motif
                                                                            hypothetical protein AT4g35800 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Experimental source: cv. Columbia R;Dietrich, M.A.; Prenger, J.P.; Gullfoyle, Ť.J. Plant Mol. Biol. 15, 207-223, 1990 A;Title: Analysis of the genes encoding the larg A;Reference number: S11960; MUID:91355869 A;Accession: S11960.
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A;Cross-references: EMBL:X52954; NID:g16504; PIDN:CAA37130.1; PID:g16505
A;Experimental source: cv. Columbia
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A; Residues: 1-1834 <BEV>
A; Cross-references: EMBL: AL031986
A; Experimental source: cultivar Columbia;
C;Accession: G85422
R;anonymous, The European Union
Nature 402, 769-777, 1999
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A; Introns: 28/3; 123/3;
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A;Note: the authors translated the codon CCT for residue 1083 as Ala
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A; Residues: 510-732, 'D',734-1055, 'R',1057-1714, 'SPTSPSY',1715-1834 <NAW2>
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Genet. 223, 65-75, 1990
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A; Residues: 1-249 <HEA>
A; Cross-references: EMBL:L76172
A; Experimental source: biotype B, isolate UQ62
A; Note: in the authors' translation residues 1-10 are
                                                                                                                                                                                                                                                                                                                                              related to finger protein XFG 68 [imported] - Neurospora crassa N;Alternate names: protein B15120.10 C;Species: Neurospora crassa C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change C;Accession: T51031
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A;Title: CgTl: a non-LTR retrotransposon with restricted distribution
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A;Experimental source: BAC clone B15120; strain OR74A
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A; Residues: 1-217 <SCH>
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A; Accession: T51031
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A; Accession: S72619
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 28
                                                                                                                                                                                                                                                         Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55 ISPVSVGRGPDP 66
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PRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSVGR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVPRWVCHPNTNTAQPTPQRQEPSPAMASQPAAGPSQGPIGLLSSMHNLPKTPPPPTSLP 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLPR-----PAAVPVPLRMQPGPAHPVLSFLRPSW---DLVSAFYSLPLAPLSPTSVP 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPDYSPSAGYSPTLPGY 1808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPD--PDAHVAVNLSRY 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSIAYSPSNARLSPASPYSPTSPNYSPTSPSYSPTSPSYS----PSSPTYSPSSPYSSGA 1791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRPAAVPVPLRMQP----GPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSVGR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RGLTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91
                                                     18.5%;
37.5%;
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34.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.1%;
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Pred. No. 5.9;
3; Mismatches 3
                                Score 77.5; DE Pred. No. 0.9; 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 78; [Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CgT1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                        DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26;
                                  21;
                                                                    2;
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                                                                    Length
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                                    Indels
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                                                                      217;
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                                                                                                                                                                                                                                                                                                                               Holland, R.;
                                  9
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                                  Gaps
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A; Status: Picc. DNA
A; Molecule type: DNA
A; Residues: 1-1110 <WIL>
A; Cross-references: EMBL: 248367; P.
A; Cross-references: cone C33B4
T8K14.10 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001
                                                                      RESULT
A96826
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T19673
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submitted to the EMBL Data Library, October 1996
a-Reference number: Z19107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: Z19160
A; Accession: T19673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein C33B4.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Ceenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T19673
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A; Introns: 53/3; 156/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-503 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A; Accession: T19319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein C15H11.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Decies: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T19319
                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Introns: 20/3; 110/3; 144/3; 341/1; 455/1; 546/1; 653/3; 934/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, February 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Coles, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: CESP:C15H11.5
A; Map position: 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: CESP:C33B4.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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298 SIPLEMRQEPG----
                                                                                                                                                                                                                                                744 HPSLPRSASTPQPIQQQQSSIPPPPPPPPPPPPPHCEPT--MVHVEFTPPSTSSVPPPPPPLP 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109
                                                                                                                                                                                                                                                                                                                           Local Similarity 28.6%; les 24; Conservation
                                                                                                                                                                                                    57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 AVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSVGR
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                                                                                           10
                                                                                                                                                                                                                                                                                         3 HSLLPRPAAVPVPLRMQ-----PGPAHPVLSFLRPSWDLVSAFYSLP-LAPLSPTSVPIS 56
                                                                                                                                                           PISSGAPPPPPPPPPGGLMHVAAS
                                                                                                                                                                                                    PVSVGRGPDPD-----AHVAVN
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17; Conserv
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se: clone C15H11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -SGWYILSAMYSLPNVPLMVMTGVIRPAEVAR
                                                                                                                                                                                                                                                                                                                                  12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Score 77; DB 2
pred. No. 2.6;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                       Score 76.5; DB 2; Pred. No. 7.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIDN:CAA88324.1; GSPDB:GN00020; CESP:C33B4.3
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                                                                                                                                                                                                    73
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                                                                                                                                                                                                                                                                                                                                    Indels
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#text_change 31-Mar-2001

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Db .
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, C. Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E. C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.
Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Fitle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
                                  Qγ
                                                                              В
                                                                                                                  Ωy
                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X78993; NID:g476045; PIDN:CAA55611.1; R;Feldmann, H.; Mannhaupt, G.; Schwarzlose, C.; Vetter, I. submitted to the Protein Sequence Database, August 1994 A;Reference number: S45927 A;Accession: S45976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Mannhaupt, G.; Stucka, R.; Ehnle, S.; Vet
Yeast 10, 1363-1381, 1994
A;Title: Analysis of a 70 kb region on the
A;Reference number: S48255; MUID:95208357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable transcription factor YBR108w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YBR0901
C;Species: Saccharomyces cerevisiae
C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jul-2000
C;Accession: S48273; 845976; S44688
B;Manchardt C:Stucks D: Fitch C: Vottor T: Foldman
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S48273
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A;Molecule type: DNA
A;Residues: 1-356 <STO>
밁
                                                                                                                                                                                                                                                                                    A;Cross-references:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-848 <MAN>
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C;Genetics:
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                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-848 <FE2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: nucleic
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                                                                                                                                                                                Query Match
Best Local
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Best Local
443
                                                                              383
                                                                                                                                                                                                                                                                 position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       272 PSVPDPIIQEAMNFA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216 PGPVLGPPYSEPGPSTPTGSIPSPS----SGFLPPIVYPPPMAPPSPSVTPTSAYWCVAK 271
                                    63
                                                                                                                  13 PVPLRMQPGPAHPV----LSFLRPSWDLVSA---FYSLPLAPLSPTSVP---ISPVSVGR 62
                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GRGPDPDAHVAVNLS
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les 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ø
                                      GPDPDAH 69
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                                                                          PVPVRMQPQPPQPMQQGNIYPIEPSLDSTGSTPHFEVTPFDPDAPAPKPKIDIPTVDVSS 442
LPPPPTH
                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acid sequence not shown
                                                                                                                                                                                                                                                                                                       EMBL: Z35977;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               976; S44688
R.; Ehnle, S.; Vetter, I.; Feldmann,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.2%;
34.7%;
                                                                                                                                                                                18.2%;
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protein YBR0901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 76; DB Pred. No. 2.2; Mismatches
                                                                                                                                                             6,
                                                                                                                                                                                                                                                                                                       NID:g536378; PID:g536379; MIPS:YBR108w
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                                                                                                                                                                                Score 76;
Pred. No.
                                                                                                                                                             Mismatches
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2.2;
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                                                                                                                                                                                                 Length 848;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
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A;Status: press. DNA
A;Molecule type: DNA
A;Residues: 1-1952 <SCH>
A;Cross-references: EMBL:AL353822; GSPDB:GN00112;
A;Cross-references: cosmid contig 15E6; strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:L24049; NID:g436017; PIDN:AAA17538.1; PID:g436021 C;Superfamily: potato leaf roll virus genome-linked protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Rathjen, J.P.; Karageorgos, L.E.; Habili, N.; Waterhouse, P.M.; Symons, R.H. Virology 198, 671-679, 1994
A;Title: Soybean dwarf luteovirus contains the third variant genome type in th A;Reference number: A49600; MUID:94120742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genome-linked protein VPg - soybean dwarf virus
C;Species: soybean dwarf virus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Sep-1999
C;Accession: D49600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
D49600
beta-adaptin homolog F8L21.170 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change C;Accession: T13029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein 15E6.220 [Imported] - Neurospora crassa C;Species: Neurospora crassa C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000 C;Accession: T48814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
T48814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, submitted to the Protein Sequence Database, April 2000 A;Reference number: Z24541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: A49600; A; Accession: D49600
                                                                                       T13029
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A; Introns: 281/3
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                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: NCSP:15E6.220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: T48814
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Best Local Similarity
Matches 24; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                              2 THSLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVP---ISPV 58
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                                                                                                                                                                             STVAAAPTP
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31.1%;
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Pred. No. 1.4;
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24-Nov-1999

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hypothetical protein KIAA0595 - human (fragment)
C;Species: Homo sapiens (man)
C;Species: O1-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
C;Date: O1-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
C;Accession: T00273
R;Nagase, T; Ishikawa, K; Miyajima, N; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.
DNA, Nes. 5, 31-39, 1998
A;Title: Prediction of the coding sequences of unidentified human genes. IX. The complet A; Reference number: Z14086; MUID:98290545
A;Accession: T00273
A;Status: preliminary; translated from GB/EMBL/DDBJ
A:Molocyle type. mBNA
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A;Residues: 1-1520 <NAG>
A;Residues: 1-1520 <NAG>
A;Cross-references: EMBL;AB011167; NID:g3043713; PIDN:BAA25521.1; PID:g3043714
A;Experimental source: brain
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Search completed: April 11, 2002, 09:30:07 Job time: 104 sec
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A; Introns: 29/3; 95/3; 133/3; 217/2; 262/3; 322/3; 353/3; 424/2; 445/3; 505/3; 536/3; 66
C; Superfamily: beta-adaptin
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A;Residues: 1-894 <BEV>
A;Residues: 1-894 <BEV>
A;Cross-references: EMBL:AL096882; GSPDB:GN00062; ATSP:F8L21.170
A;Experimental source: cultivar Columbia; BAC clone F8L21
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                                                                                                                                                                                                                                                                                                                                                                           Query Match 17.5%; Score 73; DB 2; Length 1520; Best Local Similarity 35.1%; Pred. No. 23; Matches 27; Conservative 3; Mismatches 25; Indels
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Best Local Similarity 29.6%;
Matches 24; Conservative
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                                                                                                                                                                                                                                                              710 LLARPSPPVQSVSPAVPTPPSMSAALPFPAGGLGMPP-----SLPPPPLQPPSLPLS 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    619 PGNIPQPSGRQPAPAVPA-----PVPDLLGDLMGLDNAAIVPVDDPITQSGPPLPVVVPA 673
                                                                                                                                           762 MGPVL----PDPFTHYA 774
                                                                                                                                                                                           57 -- PVSVGRGPDPDAHVA 71
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                                                                                                                                                                                                                                                                                                                        5 LLPRPA-----AVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPIS 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 PAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPIS------PV 58
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Maximum Match 100%
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length: 2000000000
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    DB
NK4R HUMAN
CBP MOUSE
YD53 SYNY3
DPOL HPBHE
PGCN MOUSE
NTC3 MOUSE
TEF5 CH1CK
CDX1 HUMAN
SM6B MOUSE
FM14 MOUSE
FM14 MOUSE
FM17 CAREL
VST1 HEVBU
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PGCN_RAT
FXB2_MOUSE
RPB1_ARATH
YBV8_YEAST
PER2_HUMAN
YC18_HUMAN
SM6B_RAT
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P55067 rattus norv
Q64733 mus musculu
P18616 arabidopsis
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Q61982
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6 arabidopsis
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ID SM6B_HUMAN
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ALIGNMENTS

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(GLCNAC) ((GLCNAC)	N-LINKED (GLCNAC) (FOTENTIAL).	(GLCNAC)	(GLCNAC)	N-LINKED (GLCNAC) (POTENTIAL).	POLY-LEU.	POLY-GLY.	SEMA.	CYTOPLASMIC (POTENTIAL).	POTENTIAL.	EXTRACELLULAR (POTENTIAL).	•	POTENTIAL.		Multigene family: Neurogenesis: Glycoprotein:							eisb-sib.c	agreement (See http://www.ic	as long as its c	There are no restrictions on	ormatics and the EMBL outstatic	pyright. It is produced through a collaboration		1	RETONGS TO THE SEMADHORIN FAMILY		A ROLE IN BOTH PERIPHERAL AND CENTRAL NERVOUS	the EMBL/GenBank/DDBJ databases.						EMAPHORIN Z) (SEMA Z).	Last annotation undate)	sequence update)	Created)

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Best Local
This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM. the European Bioinformatics Institute. There are no restriuse by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.orsend.an.email to license@ish-~**
                                                                                                                                                                                                                                          O-LINKED OLIGOSACCHARIDES (BY SIMILARITY).

O-LINKED OLIGOSACCHARIDES (BY SIMILARITY).

IPTM: TWO ISOFORMS WERE FOUND THAT PROBABLY ARISE BY PROTEOLYTIC DEGRADATION. THE LARGE ISOFORM IS PREDOMINANT IN EARLY POSTNATAL BRAIN, THE SMALL ISOFORM IS FOUND IN ADULT BRAIN.

ISIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.

SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.

ISIMILARITY: CONTAINS 2 LINK DOMAINS.

ISIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.

SIMILARITY: CONTAINS 1 SUSHI (SCR) DOMAIN.

SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
NEUROCAN CORE PROTEIN PRECURSOR (245 KDA EARLY POSTNATAL CORE
GLYCOPROTEIN) (CONTAINS: 150 KDA ADULT CORE GLYCOPROTEIN].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Friedlander D.R., Milev P., Karthikeyan L., Margolis R.K., Margolis R.U., Grumet M.; Margolis R.U., Grumet M.; "The neuronal chondroitin sulfate proteoglycan neurocan bineural cell adhesion molecules Ng-CAM/L1/NILE and N-CAM, a neuronal adhesion and neurite outgrowth.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Cell Biol. 125:669-680(1994).

-!- FUNCTION: MAY MODULATE NEURONAL ADHESION AND NEURITE GROWTH
DEVELOPMENT BY BINDING TO NEURAL CELL ADHESION MOLECULES (NG
AND N-CAM). CHONDROITIN SULFATE PROTEOGLYCAN; BINDS TO HYALU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND PARTIAL SEQU
STRAIN-SPRAGUE-DAWLEY; TISSUE-Brain;
MEDLINE-92406907; PubMed-1326557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94230574; PubMed=7513709;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rauch U., Karthikeyan L., Maurel P., Margolis R.U., Margolis R.K.; "Cloning and primary structure of neurocan, a developmentally regulated, aggregating chondroitin sulfate proteoglycan of brain."; J. Biol. Chem. 267:19536-19547(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACID.
TISSUE SPECIFICITY: EARLY POSTNATAL AND ADULT
IN KIDNEY, LUNG, LIVER AND MUSCLE.
PTM: CONTAINS MOSTLY CHONDROITIN SULFATE, BUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N
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28; Conservative
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Rodentia;
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                                                         (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 67;
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(NG-CAM
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В
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                                         Query Match
Best Local S
Matches 28
                                                                                                                                                                                                                                                                                                                                                                ProDom, PD000918; Link; 2.
SMART; SM00032; CCP; 1.
SMART; SM00034; CLECT; 1.
SMART; SM00019; EGF_CA; 1.
SMART; SM00179; EGF_CA; 1.
SMART; SM00409; EG; 1.
SMART; SM00405; LINK; 2.
                                                                                                                                                                                                                                                                                                               PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
                                                                                                                       DOMAIN
DOMAIN
DOMAIN
DISULFID
                                                                                                           CARBOHYD
CARBOHYD
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DOMAIN
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DOMAIN
                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00084; sushi; Pfam; PF00193; Xlink;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00008; EGF;
                                                                                                                                                                                                                                                                                                  EGF-like doma
                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [nterPro;
               610
52
                            4
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                            SLLPRPAAVPVPLRMQPG---PAHPVLSFLR-----PSWDLVSAFYSLPLAPLS--PT 51
              SSIPSEALSAVSLQASPGDGSPDFPIVAMLRAPKLWLLPHSTLVPNVSPIPLSPASPLPS 669
                                                                                                                                                                                                                                                                                                                                                                                                                                         PF00047;
                                                                                                                                                                                                                                                                                                                                                                                                                                PF00059; lectin_c; 1.
                                                                                                                                                                                                                                                                                     PS00615; C_TYPE_LECTIN_2; 1.
PS50041; C_TYPE_LECTIN_2; 1.
stein; Hyaluronic acid; Proteoglycan; Immu
ndomain; Calcium; Repeat; Lectin; Sushi;
                                          Similarity 35.0
28; Conservative
                                                                                                                                                                                                                                                                                                                              PS00022;
PS01186;
PS01187;
PS01241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR001304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR000436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR000538
                                                                                                                                                                                                             639
51
176
274
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1155
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1057
1125
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1185
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737
944
967
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                                                                              AA;
                                                                                                                                                                                                                                                                                                                              ASX_HYDROXYL;

EGF_1; 3.

EGF_2; 1.

EGF_CA; 1.

LINK; 2.
                                                                                    339
737
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967
1164
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1257
1246
253
253
9855
9852
1023
11154
1213
1213
252
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324
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1040
11149
11191
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11191
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EGF-like.
EGF_2.
EGF_Ca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig.
Ig_MHC.
                                                  19.5%;
                                                                               135544
                                                                                                                                                                                                                                                                                                                                                                                 like; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sushi_SCR_CCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Link.
67
                                                                           10;
                                                                                                                                                                                                                                  LINK 2.
EGF-LIKE 1.
EGF-LIKE 2, CA
C-TYPE LECTIN.
                                                 Score 81.5;
Pred. No. 1:
                                                                                                                                                                                                                                                               LINK
                                                                                                                                                                                                                                                                            NEUROCAN CORE PROTEIN.
150 KDA ADULT CORE GLYCOPROTEIN
                                                                                                                                                                                                                                                                     IG-LIKE V-TYPE
                                           Mismatches
                                                  5
                                                                                                                                                                                                                                          CALCIUM-BINDING
                                                         DВ
                                                                                                                                                                                                                                                                      DOMAIN
                                                       1:
                                                                                                                                                                                                                                                                                                  Immunoglobulin
shi; Signal.
                                           25;
                                                                                                   .) (POTENTIAL).
.) (POTENTIAL).
.) (POTENTIAL).
(CHONDROITIN SULFATE).
                                                        Length 1257;
                                           Indels
                                                                              CRC64;
                                                                                     (POTENTIAL).
                                                                                                                                                                                                                                          (POTENTIAL)
                                           17;
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                                          Gaps
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                                      Query Match
Best Local
                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
30-MAY-2000 (Rel. 3
FORKHEAD DOV
                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the Dynon-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10090;
                                                                                                                                                                                                     DNA-binding;
                                                                                                                                                                                                                                                                                                                                  EMBL; X92591; CAA63335.1;
EMBL; X71942; CAA50744.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kaestner K.H., Schuetz G., Monaghan A.P.;
"Expression of the winged helix genes fkh-4 and fkh-5 defines domains
in the central nervous system.";
                                                                                                                                        DOMAIN
                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                             PROSITE; PS00658; FORK_HEAD_1; PROSITE; PS00658; FORK_HEAD_2;
                                                                                                                                                                                                                                                        SMART;
                                                                                                                                                                                                                                                                     PRINTS;
                                                                                                                                                                                                                                                                                InterPro; IPR001766; Fork_head
Pfam; PF00250; Fork_head; 1.
                                                                                                                                                                                                                                                                                                         TRANSFAC; T02442; -. MGD; MGI:1347468; Foxb2.
                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Six members of the mouse forkhead gene family are developmentally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kaestner K.H., Lee K.H., Schloendorff J., Hiemisch H.,
Monaghan A.P., Schuetz G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FORKHEAD
                                                                                                                  DOMAIN
                                                                                                                                                       DOMAIN
                                                                                                                                                                 DOMAIN
                                                                                                                                                                                           DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            regulated.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93361500; PubMed=7689224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 4-114 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mech. Dev. 55:221-230(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97014266; PubMed=8861101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FOXB2 OR FKH4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FXB2_MOUSE
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670 SVPEEQAVRPVSFG-AEDPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         !- DEVELOPMENTAL STAGE: EXPRESSED DURING EMBRYOGENESIS.
3 HSLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLP-----LAPLSPTSVPIS 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                         SM00339; FH; 1.
                                      Similarity
                                                                                                                                                                                                                                                                     PR00053;
                                                                                                                                                                                                                     PS50039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                997 (Rel. 35, Created)
997 (Rel. 35, Last sequence update)
900 (Rel. 39, Last annotation update)
BOX PROTEIN B2 (TRANSCRIPTION FACTOR
                                                                                  Acad. Sci. U.S.A. 90:7628-7631(1993).
                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                     FORKHEAD.
                                                                                                                                                                                                                    FORK_HEAD_3;
                                                                                                                                                                                                                                          FORK_HEAD_1;
                                   19.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 889
                         10;
                                                                                                                                                                                                                                                                                                                                                                                                is not removed.
                                     Score 80; DB 1
Pred. No. 0.68;
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                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    428
                                                 DB 1;
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                         25;
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                                               Length 428
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RPB1_AF
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RA Van der Schueren J., Grymonpez B., Chuang Y.-J., Vandenbussche F.,
RA Braeken M., Weltjens I., Voet M., Bastlaens I., Aert R., Defoor E.,
RA Braeken M., Weltjens I., Voet M., Bastlaens I., Aert R., Defoor E.,
RA Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Mocijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Mocijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Mocijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Mocijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Mocijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Mocijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Mocijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA De Keyser A., Buysshaert C., Gielen J., Vilalen S., Van den Daele H.,
RA Van Montagu M., Rogers J., Cronin A., Daular N., McLay K., Mayes R.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
RA Clark L., Rajandream M.-A., Lyne M., Benes V., Rechmann S.,
RA Pettett A., Rajandream M.-A., Lyne M., Benes V., Rechmann S.,
RA Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H.,
RA Borkova D., Bloecker H., Scharfe M., Granderath K., Dauner D., Herzl A.,
RA Gabel C., Fuchs M., Fattmann B., Granderath K., Dauner D., Herzl A.,
RA Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RPB1_ARATH
P18616; P316
01-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G., Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N., Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M., Weichselgartner M., de Simone V., Obermaler B., Mache R., Mueller M., Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T., Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I., Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P., Langham S.-A., McCullagh B., Bilham L., Robben J., Langham S.-A., McCullagh B., Bilham L., Robben J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1990 (Rel. 16, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (
RPB205 OR RPII OR RPB1 OR AT4G35800 OR F4B14.70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAINECV. COLUMBIA;
MEDLINE=91080867; PubMed=2259344;
Nawrath C., Schell J., Koncz C.;
"Homologous domains of the largest subunit of polymerase II are conserved in plants.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20083488; PubMed=10617198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Dietrich M.A., Prenger J.P., Guilfoyle T.J.;
"Analysis of the genes encoding the largest subunit of RNA polymerase II in Arabidopsis and Soybean.";
Plant Mol. Biol. 15:207-223(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CV. COLUMBIA; MEDLINE=91355869; Pu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          408 PTAAGR 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P31635; Q9SZS8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COLUMBIA;
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XA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,

A Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,

XA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,

XA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,

XA Minx P., Bentley D., Fulton B., Miller N., Pepin K., Hillier L.,

XA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,

XA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,

XA Nelson J., Berghoff A., Jones K., Drone K., Cotton M., Jóshu C.,

XA Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,

XA Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,

XA Antonoiu B., Zidanic M., Rofriguez M., Hoffman J., Till S.,

XA Antonoiu S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,

XA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,

XA Chen E., Marra M., Martienssen R., McCombie W.R.;

**Sequence and analysis of chromosome 4 of the plant Arabidopsis
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Nature 402:769-777(1999).

-i- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X52954; CAA37130.1; -. 

EMBL; X52494; CAA36735.1; -. 

EMBL; AL031986; CAA21466.2; -. 

EMBL; AL161588; CAB81489.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).
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InterPro; IPR000684; RNA_polII_repeat.
InterPro; IPR000722; RNA_pol_A.
InterPro; IPR002879; RNA_pol_A2.
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PTM: THE TANDEM 7 RESIDUES REPEATS CAN BE HIGHLY PHOSPHORYLATED.

THE PHOSPHORYLATION ACTIVATES POL2.

MISCELLANEOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES WERE FOUND IN EURARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA PRECURSOR, POLYMERASE II FOR THE MENA PRECURSOR, POLYMERASE II FOR THE MENA PRECURSOR, ADLYMERASE II FOR THE MENA PRECURSOR, ADLYMERASE SILI FOR SS AND TRAN GENES.

SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
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PS00115; RNA_POL_II_REPEAT; 23.
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20-AUG-2001 (Rel. 40, Last

PERIOD CIRCADIAN PROTEIN 2

PER2 OR KIAA0347

Homo sapiens (Human)
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SGD; S0000312; YBR108W.
Hypothetical protein.
SEQUENCE 848 AA; 92762 MW;
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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 Eukaryota; Metazoa;
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 Chordata; Craniata; Vertebrata; Euteleostomi;
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FACTOR. BEHAVES AS A NEGATIVE ELEMENT IN CIRCADIAN TRANSCRIPTIONAL
LOOP. DOES NOT APPEAR TO BIND DNA, SUGGESTING INDIRECT
TRANSCRIPTIONAL INHIBITION. EXPRESSION OSCILLATES WITH A 24 HR
RHYTHM IN THE SUPRACHIASMATIC NUCLEUS (SCN) AND THE WHOLE EYES.
OSCILLATIONS ARE MAINTAINED UNDER CONSTANT DARKNESS AND ARE
RESPONSIVE TO CHANGES OF THE LIGHT/DARK CYCLES. THERE IS A 4 HOUR
TIME DELAY BETWEEN ERRI AND PERZ OSCILLATIONS. THE EXPRESSION
RHYTHMS APPEAR TO ORIGINATE FROM RETINA (BY SIMILARITY).

-!- SUBCELULAR LOCATION: NUCLEAR (POTENTIAL).

-!- TISSUE SPECIFICITY: WIDELY EXPRESSED. FOUND IN HEART, BRAIN,
PLACENTA, LUNG, LIVER, SKELETAL MUSCLE, KIDNEY AND PANCREAS.
-!- INDUCTION: BY LIGHT (BY SIMILARITY).

-!- SIMILARITY: CONTAINS 1 PAS (PER-ARNT-SIM) DIMERIZATION DOMAIN.
-!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
                                                                                                          DOMAIN
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97349984; PubMed=9205841;
Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. VI
The complete sequences of 100 new cDNA clones from brain which can
code for large proteins in vitro.";
DNA Res. 4:141-150(1997).
                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                           MIM; 603426;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nagase T., Ishikawa K.-I., Seki N., Nakajima D., Ohira
Miyajima N., Kotani H., Nomura N., Ohara O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Brain
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Neuron 19:1261-1269(1997)
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                                                                                                                                                                                                                                                                                          InterPro; IPR001610; PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Two period homologs: circadian expression and
                                              Local
 1 GTHSLLPRP-----AAVPVPLRMQ------PGPAHPVLSFLRPSWDLVSAFYSLPL 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSCRIPTION FACTORS.
                              l Similarity
30; Conserv
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                                Conservative
                                                                                                                                                                                                                                 regulation;
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                                             17.8%;
                                                                                                                                                                                                                                                                              PAS.
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                                                                                                           136579
                                                                                                                                                                                                                 Nuclear protein; Repeat; Biological rhythms HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
                                10;
                                                                                                                     PAS-1.
PAS-2.
PAC MOTIF.
POLY-ARG.
NUCLEAR LOCALIZATION SIGNAL.
PRO-RICH.
                                                                                                          MW;
                                                                                                                                                                                                                                                                                                                           ALT_INIT.
                              Score 74.5; D
Pred. No. 7.2;
O; Mismatches
                                                                                                          2AEF2C6BD4B6CBB0 CRC64;
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YC18_HUMAN
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Best Local
                                   SM6B_RAT
070141;
30-MAY-2000
30-MAY-2000
20-AUG-2001
                                                                                                                                                                                                                                                                                                                      DOMAIN
DOMAIN
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
Rattus norvegicus (Rat)
             SEMAPHORIN SEMA6B.
                                                                                                     RAT
                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB033044; BAA86532.1; -.
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Nagase T., Ishikawa
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20-AUG-2001 (Rel. 40, Last sec
20-AUG-2001 (Rel. 40, Last and
HYPOTHETICAL PROTEIN KIAA1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9ULK2;
                                                                                                                                                                                                                                                                                                                                                                         Hypothetical
NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ohara O.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE ATAXIN 7 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         large proteins in vitro."; Res. 6:337-345(1999).
                                                                                                                                                                                                                   SLLPRPAA---VPVPLR-MQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSP------
                                                                                                                                                                   SVPISPVSVGRGPDPDA-----HVAVNLS 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTVAAPPAPPHASFTVPAVPVDLQHQFAVQPPPFPAPLAPVMAFMLPSYSFPSGTPNLPQ 922
                                                                                                                                                     SAMLSNAAFVTSPDPSALMSHTTAFPHVAATLS
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                     O (Rel. 39, Created)
O (Rel. 39, Last sequence update)
I (Rel. 40, Last annotation update)
6B PRECURSOR (SEMAPHORIN Z) (SEMA Z).
                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                     protein.
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                                                                                       STANDARD;
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wa K.-I., Kikuno R.,
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664 F
790 F
92138 MW;
                                                                                                                                                                                                                                                                   17.6%;
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POLY-SER.
POLY-SER.
; DE5CE8130E48DA23 CRC64;
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RESULT 9

NK4R_HUMAN
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Best Local :
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NK4R_HUMAN
P30098;
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20-AUG-2001
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                                                                                                                                                                                                                                                                                                                               SMART; SM00423;
                                                                                                                                                                                                                                                                                                                                      .Pfam; PF01403; Sema;
                                                                                                                                                                                                                                                                                                                                             EMBL; AB000776; BAA25687.1; -.
InterPro; IPR003659; PSI.
InterPro; IPR001627; Sema.
                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
                                                                                                                                                                                                                                                                                                                                                                                                                                    This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            semaphorin Z.";
Brain Res. Mol. Brain Res. 51:229
-!- FUNCTION: MAY PLAY A ROLE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=WISTAR; TISSUE=Brain; MEDLINE=98087397; PubMed=9427525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10116;
                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular cloning of a novel member of semaphorin
                                                                                                                699
                                                                                              52
                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

DEVELOPMENTAL STAGE: DETECTED IN THE FIRST BRANCHIAL ARCH

EMBRYONIC DAY 11 (E11) EMBRYO, AND SUBSEQUENTLY IN THE MYC

AND THE DORSAL ROOT GANGLIA IN DEVELOPING SOMITES FROM E11

THROUGH E13.5, BUT NOT IN THE BRAIN. HOWEVER, AT E15, 18,

PO, SEMAZ WAS HIGHLY EXPRESSED IN THE BRAIN.

SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.

SIMILARITY: CONTAINS 1 SEMA DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYSTEM DEVELOPMENT
                                                                                                                        GTH----SLLPRPAAVPVPLRMQPGPAHPVLSFLRP-SWD----LVSAFYSLPLAPLSPT
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                                                                                                               GPHDLDSGLLPTPEQTPLPQKRLP-TTHPHAHALGPRAWDHSHALLSASASTSLLLLAHT
                                                                              RAPEQPPVPTESGPE
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                                   STANDARD;
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387
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Rodentia;
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Last sequence update)
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Pred. No. 6.3;
                                                                                                                                                                                                                                                                    POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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                                   PRT;
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TRANSMEM
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GCRDb; GCR_0377; --
Therpro; IPR000276; GPCR_Rhodpsn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHARACTERIZATION. MEDLINE-97103087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Placenta;
MEDLINE=92237319;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEUROMEDIN K RECEPTOR (NKR) (NK-4R) (K1R) (NEUROKININ 4 TACR3L OR TAC3RL OR TC4R.
                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR00244; NEUROKININR.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cloned tachykinin peptide receptor.";
Biochem. J. 320:1-5(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Donaldson L.F., Haskell C.A., Hanley M.R.; "Functional characterization by heterologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M84605; AAA36395.1; -.
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Xie G.-X., Miyajima A., Goldstein A.;
"Expression cloning of cDNA encoding a seven-helix
human placenta with affinity for opioid ligands.";
Proc. Natl. Acad. Sci. U.S.A. 89:4124-4128(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE SPECIFICITY: HIGHEST LEVELS IN SKELETAL MUSCLE, LIVER, LUNG AND HEART. LOW LEVELS IN PANCREAS.

SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. HIGHEST TO OTHER TACHYKININS RECEPTORS.

CAUTION: WAS ORIGINALLY THOUGHT TO BE A KAPPA-TYPE OPIOID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: THIS IS A RECEPTOR FOR THE TACHYKININ NEUROPEPTIDE NEUROMEDIN K (NEUROKININ B). THE RANK ORDER OF AFFINITY OF THIS RECEPTOR TO TACHYKININS IS: NEUROMEDIN K > SUBSTANCE K > SUBSTANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
TISSUE SPECIFICITY: HIGHEST LEVELS IN SKELETAL MUSCLE, LIVER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A44081;
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N_RECEP_F1_2; 1.
Transmembrane;
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              CYTOPLASMIC (POTENTIAL).
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PALMITATE (BY SIMILARITY).
                                                                                                           7 (POTENTIAL)
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                                                                                                                                                                                 EXTRACELLULAR 5 (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Phosphorylated CREB binds specifically to the nuclear protein CBP.";
Nature 365:855-859(1993).
-i- FUNCTION: MEDIATES CAMP-GENE REGULATION BY BINDING SPECIFICALLY TO
PHOSPHORYLATED CREB PROTEIN. ACTING AS A COACTIVATOR, CBP AUGMENTS
THE ACTIVITY OF PHOSPHORYLATED CREB TO ACTIVATE TRANSCRIPTION OF
                                                                                                                                                                                                                                                                                       SMART; SM00297; BROMO; 1
SMART; SM00291; ZnF_ZZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-FEB-1996 (Rel. 33, Last seq
15-JUL-1998 (Rel. 36, Last ann
CREB-BINDING PROTEIN.
                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                    Transcription
                                                                                                                                                                                                                                        PROSITE; PS00633; BROMODOMAIN_1; 1. PROSITE; PS50014; BROMODOMAIN_2; 1.
                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00503;
                                                                                                                                                                                                                                                                                                                                                          Pfam; PF02135; zf-TAZ; 2. Pfam; PF00569; ZZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001487; Bromodomain.
InterPro; IPR003101; KIX.
InterPro; IPR000197; TAZ_finger.
InterPro; IPR000433; ZnP_ZZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSFAC; T01318;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=94019866; PubMed=8413673;
Chrivia J.C., Kwok R.P.S., Lamb N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
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SIMILARITY: CONTAINS 1 BROMODOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                         PF00439; bromodomain; 1. PF02172; KIX; 1.
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Rodentia;
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POLY-GLN.
POLY-GLN.
POLY-GLN.
POLY-GLN.
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                                                                                                                                                                                            lear protein;
BROMODOMAIN.
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    OABB028C3112F419 CRC64;
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                                                                                                                                                                                                                  Activator; Bromodomain
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55 ISPVSVGRGPD-PDAHVAVN 73

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SLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWD--LVSAFYSLP--LAPLSPT----SVP 54

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20-AUG-2001
                                                                                                                                    use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for entities requires a license agreement.
                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                           "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synechocystis sp.
                                                                 Hypothetical SEQUENCE 2
                                                                                       EMBL; D10716; BAA38818.1; -. EMBL; D90912; BAA18174.1; -.
                                                                                                                                                                                                                                                                                   Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                 Malakhov M.P., Wada H., Los D.A., Sakamoto T., Murata N., "Structure of a cyanobacterial gene encoding the 50S ribosomal protein L9.";
                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Cyanobacteria;
NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL
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                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                DNA Res. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                    Kaneko T., Sato S.,
                                                                                                                                                                                                                                                                                                                                                MEDLINE=97061201; PubMed=8905231;
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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  l Similarity
23; Conser
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291 AA; 31283 MW;
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L 31.3
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. 32, Last sequ
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              16.9%;
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36.5%;
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PROTEIN SLR1353.
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  16;
Score 70.5; DB
Pred. No. 3.8;
16; Mismatches
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5AB7E3DD03C36390 CRC64;
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              70.5;
No. 3.
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No. 28;
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                          DB 1;
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RESULT 12
DPOL_HPBHE
RRP OCC OR DET
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PGCN_MOUSE
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Best Local
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P55066;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last seque
20-AUG-2001 (Rel. 40, Last annot)
NEUROCAN CORE PROTEIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pl384b;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-JAN-1990 (Rel. 13, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
P PROTEIN [INCLUDES: DNA-DIRECTED DNA POLYMERASE (EC 2.7.7.7); RNA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DPOL_HPBHE P13846;
                                  Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                          Pfam; PF00336; DNA_pol_viral_C; 1.
Pfam; PF00242; DNA_pol_viral_N; 1.
Pfam; PF00078; rvt; 1.
                                                                                                                                                                                                                                                                                                                    PIR; A30082; JDVLHH.
InterPro; IPR001462; DNApol_viral_C.
InterPro; IPR000201; DNApol_viral_N.
InterPro; IPR000477; RVTse.
                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                   ProDom; PD000814; DNApol_viral_C; 1.
Transferase; RNA-directed DNA polymerase; DNA-directed DNA polymerase; Hydrolase; Nuclease; Endonuclease; DNA replication; DNA-binding.
SEQUENCE 788 AA; 90070 MW; FB44F38F75EADF44 CRC64;
                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is between the Swiss Institute of Bioinformatics Institute. The European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-88333160; PubMed=3418788;
Sprengel R., Kaleta E.F., Will H.;
"Isolation and characterization of
STRAIN-BALB/C;
        SEQUENCE FROM N.A
                                                                CSPG3 OR NCAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Virol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  herons.";
                         NCBI_TaxID=10090;
                                                                                                                                                                     444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heron hepatitis b virus
                                                                                                                                                                                      31 RPSWDLVSAFYSLPLAPLSPTSVPIS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: ENDONUCLEOLYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Virol. 62:3832-3839(1988).
CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE
N PYROPHOSPHATE + DNA(N).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MONOESTER.
                                                                                                                                                                    RISLDLSQAFYHLPLAPASSSRLAVSDGKQVYYFRKAPMGVGLSP 488
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                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                          Conservative
TISSUE-Brain;
                                   Chordata;
Rodentia;
                                                                                                                                                                                                                 16.9%;
                                                                        Last sequence up Last annotation PRECURSOR.
                                                                                                                                                                                                        Score 70.5; Di
Pred. No. 11;
4; Mismatches
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                                  Craniata; Ver
Sciurognathi;
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(See http://www.isb-sib.ch/announce/
                                                                                update)
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                                             Vertebrata; Euteleostomi;
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                                   Muridae;
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                                   Murinae;
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Pfam; PF00193; Xlink; 2.
ProDom; PD00918; Link; 2.
SMART; SM00034; CCP; 1.
SMART; SM00034; CLECT; 1.
SMART; SM00079; EGF_CA; 1.
SMART; SM00001; EGF_Like; 1.
SMART; SM00409; IG; 1.
SMART; SM00409; IG; 1.
              DOMAIN
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PROSITE;
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InterPro;
InterPro;
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-i- FUNCTION: MAY MODULATE NEURONAL ADHESION AND NEUF
                                                                                                                         DOMAIN
DOMAIN
                                                                                                                                                                                     CHAIN
DOMAIN
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contents the statement is not removed.
                                                                                                                                                                                                                                  Glycoprotein; EGF-like doma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96039250; PubMed=7490074; Rauch U., Grimpe B., Kulbe G., Ar
                                                                                                            DOMAIN
                                                                                                                                                         DOMAIN
                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                     SIGNAL
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SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V
SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.

SIMILARITY: CONTAINS 2 LINK DOMAINS.

SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY
SIMILARITY: CONTAINS 1 SUSHI (SCR) DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGI:104694;
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B; PS00010; ASX_HYDROXYL; ]

B; PS00022; EGF_1; 3.

B; PS01186; EGF_2; 1.

B; PS01187; EGF_CA; 1.

B; PS01241; LINK; 2.

B; PS01241; LINK; 2.
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| IPRO00561; EGF-11ke.
| IPRO00742; EGF_2.
| IPR00181; EGF_Ca.
| IPR003599; Ig.
                                                                                                                                                                                                                                                PS00615; C_TYPE_LECTIN_1; 1.
PS50041; C_TYPE_LECTIN_2; 1.
ptein; Hyaluronic acid; Proteoglycan;
                                                                                                                                                                                                                                       domain;
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3; Xlink; 2.
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Ig_MHC.
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C-TYPE LECTIN.
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EGF-LIKE 2,
                                                                                                                                                                                     NEUROCAN CORE PROTEIN. IG-LIKE V-TYPE DOMAIN.
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                                                                                                                                                                                                                                   Sushi;
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RESULT 14
NTC3_MOUSE
ID .NC7C3_M
AC 061982
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DT 01-NOV
DT 20-AUG
DE *NEUROG
GN NOTCH3
OC ELMANY
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Best Loc
Matches
                                                                                                                                                                                                                                                                         PROUVELLE AT THE DECISIONS AND MORHOLOGICAL MOVEMENTS IN TO DEVELOPING CNS AND PROBABLY OTHER REGIONS OF THE EMBRYO.

1 TISSUE SPECIFICITY: PROLIFERATING NEGROEPITHELIUM.

1 DEVELOPING THE STAGE: CNS DEVELOPMENT.

1 DEVELOPMENTAL STAGE: CNS DEVELOPMENT.

1 SIMILARITY: CONTAINS 34 EGF-LIKE DOMAINS.

1 SIMILARITY: CONTAINS 5 ANK REPEATS.

1 SIMILARITY: CONTAINS 5 ANK REPEATS.
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Q61982;
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Eukaryota; Metazoa; (
Mammalia; Eutheria; I
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-ICR X SWISS WEBSTER;
MEDLINE-95001556; PubMed-7918097;
Lardelli M., Dalstrand J., Lendahl U.;
"The novel Notch homologue mouse Notch"
"The novel Notch homologue mouse Notch"
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neuroepithelium.";
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                                                                                                                                  equires a license agreemer email to license@isb-sib.
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Rodentia;
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26.1%;
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(See http://www.isb-sib.ch/announce/
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Pfam; PF00006; notch; 3.
PRINTS; PR00010; EGFBLOOD.
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SMART; SM00179; EGF_CA; 19.
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PROSITE; PS0008; ANK_REPEAT; 4.
PROSITE; PS50097; ANK_REPEAT; 4.
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Matches 2
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A Zakie A., Larkin S.B., Farrance I.K., Grenningloh G., Or A Zakie A., Larkin S.B., Farrance I.K., Grenningloh G., Or MINTER J. a novel member of the transcription enhancer fac (TEF-1) multigene family.";

J. Biol. Chem. 271:8360-8365(1996).

J. Biol. Chem. 271:8360-8365(1996).

C -!- FUNCTION: SEQUENCE SPECIFIC M-CAT-BINDING FACTOR.

C -!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).

C -!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).

C -!- SUBCELLULAR FRODUCTS: 2 ISOFORMS; DTEF-1A (SHOWN HERE IB); ARE PRODUCTS: 1 ISOFORMS; DTEF-1A (SHOWN HERE IB); ARE PRODUCTS: 1 ISOFORMS; DTEF-1A (SHOWN HERE IB); ARE PRODUCTS: 1 INCARDIAC MUSCLE, LOUMUSCLE. INTERNATIVE SPLICING.
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Q90701; Q90702;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence upda
30-MAX-2000 (Rel. 39, Last annotation up
TRANSCRIPTION ENHANCER FACTOR TEF-5 (
TRANSCRIPTION FACTOR 1) (DTEF-1).
TEF5 OR DTEF1.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata;
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                                                                                                               This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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PROSITE; PS00554; TE/
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EMBL; U46128; AAC59787.1;
InterPro; IPR000818; TEA.
Pfam; PF01285; TEA; 1.
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MEDLINE=96215227;
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Gallus.
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 on:
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418
1 GTHSLLPRPAAVPV
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Gapop 10.0 ,
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Copyright (c) 1993 - 2000 Com
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285.674 Million cell updates/sec
      O9xdh2 mycobacteri
O9r172 rattus norv
O9p310 neurospora
O9vi97 drosophila
O911c8 streptomyce
O36612 swine hepat
O17585 caenorhabdi
O09493 caenorhabdi
O99671 schizosacch
                                                                                               Q99jk6 mus musculu
Q99ul5 theileria p
Q90ul5 mus musculu
Q90ul6 rathus norv
Q99ul6 arabidopsis
Q9imy0 cercopithic
Q99ul6 hapatitis e
                                                                                                                                                                                 Q9uk79 homo sapien
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	17.2	17.2	17.2	17.2	17.3	17.3	17.3	17.3	17.5	17.5	17.5	17.5	17.5	17.5	17.6	17.6	17.6	17.7	17.8	17,.8	17.9	17.9	17.9	17.9	17.9	18.2
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	Q91008	Q9QCX4	09в0с3	071146	015047	Q9GRM9	Q9F9V7	053738	Q24292	Q9BZE5	Q9Y4E0	Q9VRM2	Q9H9M1	Q9WLK2	Q9DGT6	Q9P1V7	Q9BTQ8	Q9D789	Q9M650	Q9SUS3	Q9P6T1	Q9H8F3	Q9KXQ7	Q87034	Q08404	Q9NXC6
	Q91008 gallus gall	Q9qcx4 chayote mos	Q9bqc3 homo sapien	071146 hepatitis e		Q9grm9 leishmania	Q9f9v7 mycobacteri	O53738 mycobacteri	Q24292 drosophila	homo		Q9vrm2 drosophila			Q9dgt6 turkey herp	Q9plv7 homo sapien	Q9btq8 homo sapien	Q9d789 mus musculu	Q9m650 arabidopsis	Q9sus3 arabidopsis	Q9p6tl neurospora	Q9h8f3 homo sapien	Q9kxq7 streptomyce	Q87034 soybean dwa	Q08404 soybean dwa	Q9nxc6 homo sapien

ALIGNMENTS

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Matches 77
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Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF177761; AAD56009.2; -
InterPro; IPR000494; EGFR L.
InterPro; IPR002174; Furin-like.
Pfam; PF00757; Furin-like; 1.
Pfam; PF00757; Furin-like; 1.
SMART; SM00261; FU; 1.
SMART; SM00261; FU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The HER-2/neu receptor tyrosine kinase autoinhibitor.";
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O9UK79; PRELIMINARY;
O1-MAY-2000 (TIEMBLrel. 13,
O1-MAR-2001 (TIEMBLrel. 16,
O1-JUN-2001 (TIEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=99415951; PubMed=10485918;
Doherty J.K., Bond C., Jardim A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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   61 GRGPDPDAHVAVNLSRYEG 79
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                                                                                                       GTHSLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSV 60
                                                                 GTHSLPPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSV 400
                                                                                                                                                                                                 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sci. U.S.A. 96:10869-10874(1999)
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97.5%;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                             Score 406; DB 4;
Pred. No. 4.2e-34;
1; Mismatches 1
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Submitted (APR-2001)
EMBL; BC006054; AAHONNON_TER 1
                                                                                                                                                                                                                                                                                                  Bishop R., Gobright E., Nene V., Morzaria S., Musoke A., Sohanpal "Polymorphic open reading frames encoding secretory proteins are located less than 3 kilobases from Theileria parva telomeres."; Mol. Biochem. Parasitol. 110:359-371(2000).

EMBL; AF225701; AAG28022.1; "InterPro; IPR002965; P_rich_extensn.
PRINTS; PRO1217; PRICHEXTENSN.

Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
PubMed=11071289;
Bishop R., Gobrigh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Alveolata; Apicomplexa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
17-101-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
UNKNOWN (PROTEIN FOR IMAGE:3591061) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Theileria parva.
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                                                     159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142
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                                                                             SLLPRPAAVPV--PLRMQPG-PAHPVLSFLRPSWDLVSAF-----YSLPLAPLSPTSVPI 55
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  SPVSVGRGPDPDAHVAVNLSRYEG
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Rodentia;
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Pred. No. 0.53
11; Mismatches
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                                                   -PRYPQVSGYSPYHPYARPPSPVQPIPPPS
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                                                                                                                                                                                                   Length 434;
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                                                   213
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O35615;
01-JAN-1998 (Tremblrel. 0
01-JAN-1998 (Tremblrel. 0
01-JUN-2001 (Tremblrel. 1
                                                                                                                                                                                                                                                                                                                                                                            070474
070474;
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01-AUG-1998 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
EMBL;
HSSP;
                    STRAIN-SPRAGUE-DAWLEY; TISSUE-HIPPOCAMPUS; Zachmann-Brand B., Schaller H.C.; Submitted (APR-1998) to the EMBL/GenBank/DDBJ EMBL; AF060879; AAC15766.1; -.
                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0048; ZINCFINGER.

SMART; SM00355; ZnF_C2H2; 5.

PROSITE; PS00037, MYB_1; UNKNOWN_1.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_2.

PROSITE; PS00157; ZINC_FINGER_C2H2_2; 2.

PROSITE; PS50157; ZINC_FINGER_C2H2_2; 2.

DNA-binding; Nuclear protech; Zinc-finger.

SEQUENCE 995 AA; 105983 MW; 293255B28151ECB8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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InterPro; IPR001005; Myb_DNA_bind.
InterPro; IPR000822; Znf-C2H2.
Pfam; PF00096; Zf-C2H2; 9.
                                                                                                                                                                                                                                                                           NEUROCAN (FRAGMENT)
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EMBL; AF006492; AAC53292.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRIEND OF GATA-1
                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                         NCBI_TaxID=10116;
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Pred. No. 1.4;
10; Mismatches
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Last sequence update)
Last annotation update)
                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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InterPro;

IPR000742; IPR001881; IPR000152; IPR000561;

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RESULT
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                                                                                     STRAIN-CY. COLUMBIA;

STRAIN-CY. COLUMBIA;

STRAIN-CY. COLUMBIA;

Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,

Shen M., Ronning C.M., Fraser C.M., Somerville C.R., Venter J.C.;

"Arabidopsis thaliana chromosome II BAC T16B12 genomic sequence.";

Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AC005311; AAC63847.1; -.

HSSP; P00303; ZCBP

InterPro; IPR003245; Cu_bind_like.

Pfam; PP02298; Cu_bind_like; 1.

ProDom; PD003122; Cu_bind_like; 1.

SEQUENCE 200 AA; 21475 MW; E6659011C997E349C CRC64;
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082761;
01-NOV-1998 (TREMBLRE1. 0
01-NOV-1998 (TREMBLRE1. 0
01-JUN-2001 (TREMBLRE1. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
PROSITE; PS00022; EGF_1; UNKNOWN_3.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01187; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
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SMART; SM00179; EGF_CA; 1.
SMART; SM00001; EGF_like; 1.
SMART; SM00445; LINK; 1.
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PF00193; Xlink; 1.
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       Conservative
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EGF_Ca.
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                     Score 81; [
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A Liu S.X., Sakano H., Yu G., Etgu P., Lee J., Lenz C., Pham P.,

A Toriumi M., Chan A., Chung M., Goldsmith A., Liu A., Smith A.,

A Vaysberg M., Altafi H., Brooks S., Buehler E., Chao Q., Conn L.,

A Conway A.B., Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B.

RA Miranda M., Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W.

RA Ecker J.R., Federspiel N.A., Theologis A.;

RT "The sequence of BAC F742 from Arabidopsis thaliana chromosome 1.";

RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AC034256; AAF82153.1; -.

DR InterPro; IPR002965; P_rich extensn.

DR PRINTS: PR01217; PRICHEXTENSN.

SQ SEQUENCE 1006 AA; 103943 MW; C9FB49F9930C238D CRC64;
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Best Local
STRAIN=LCL8664;
STRAIN=LCL8664;
MEDLINE=20304984; PubMed=10846073;
Jiang H., Cho Y.-G., Wang F.;
"Structural, Functional, and Genetic Comparisons
"Structural, Functional, and 3C Homologs Encoded 1
                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9IMYO;
                                                                                                                                                                                                           Gammaherpesvirinae;
NCBI_TaxID=104228;
                                                                                                                                                                                                                                                             Cercopithicine herpesvirus 15.
Viruses; dsDNA viruses, no RNA
                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation updat
LATENT NUCLEAR ANTIGEN EBNA-3A.
                                                                                                                                                                SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                  EBNA-3A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eueurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9LMQ1;
01-OCT-2000
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01-JUN-2001
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22; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                     Lymphocryptovirus
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15,
17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 81; DB; Pred. No. 2.9; 5; Mismatches
                                                                                                                                                                                                                                                                RNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation updat
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7.9;
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                                  Epstein-Barr
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Davis R.W.,
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RESULT
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Hypothetical
SEQUENCE 12
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01-MAY-1999
01-JUN-2001
Q9XDH2
Q9XDH2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-99190429; PubMed-10092008; Erker J.C., Desai S.M., Schlauder G.G., Dawson G.J., "A hepatitis E virus variant from the United States: characterization and transmission in cynomolgus macaq J. Gen. Virol. 80:681-690(1999).
EMBL; AF060669; AAD15817.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lymphocryptovirus.";
J. Virol. 74:5921-5932(2000).
EMBL; AF159308; AAF78881.1; ~.
SEQUENCE 955 AA; 104700 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schlauder G.G., Dawson G.J., Erker J.C., Kwo P.Y., Knig Smalley D.L., Rosenblatt J.E., Desai S.M., Mushahwar I. "The sequence and phylogenetic analysis of a novel hepaisolated from a patient with acute hepatitis reported i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-HEV-US2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; ssRNA positive-strand viruses,
NCBI_TaxID=12461;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                States.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
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                                                                                                                                                                                                                                                                                                                                      Match
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                                                                                                                                                                                                           GVTGLILSPS--PSPIFIQPTPS-PPMSFHNPGLELALDSRPAPLXPLGVTSPSAPPLPP
                                                                                                                                                                                                                                                  GTHSLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPL---SPTSVPISP 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Pro; IPR003384; HEV_ORF2.
PF02444; HEV_ORF2; 1.
                                                                                                                                                                                                                                                                                           ch 18.7%;
l Similarity 36.1%;
22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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122 AA; 1
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(TrEMBLrel. 10,
(TrEMBLrel. 17,
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                       PRELIMINARY;
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31.9%;
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                                                                                                                                                                                                                                                                                           Score 78; DB
Pred. No. 0.67
LO; Mismatches
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                  26DDFE0757065BE0
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                                                                                                                                                                                                                                                                                               23;
                                                                                                                                                                                                                                                                                                                                                                                                  CRC64;
                                                                                                                                                                                                                                                                                                                               Length 122;
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the United
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RESULT
Q9R172
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Best Local
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O9R172;
01-MAY-2000 (TrEMBLrel. 1
01-MAR-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
                                                                                InterPro;
InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Espitia C., Laclette J.L., Mondragon-Palomino M., Martens A.,
Zhang Y., Moreno C., Singh M.;
"Cloning and characterization of a new member of the PGRS family that
is a useful marker of polymorphism in Mycobacterium tuberculosis.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF071081; AAD41594.1;
InterPro; IPR002951; Atrophin.
InterPro; IPR002951; Arrophin.
InterPro; IPR003952; P.rich_extensn.
InterPro; IPR003882; Pistil_extensin.
PRINTS; PR01212; ATROPHIN.
PRINTS; PR01212; ATROPHIN.
PRINTS; PR01218; PSTLEXTENSIN.
PRINTS; PR01218; PSTLEXTENSIN.
PRINTS; PR01218; PSTLEXTENSIN.
PSTLEXTENSIN.
39168EC45A5916F8 CRC64;
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                                                                                                                                            InterPro;
InterPro;
                                                                                                                                                                                 EMBL;
HSSP;
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Bacteria; Firmicutes; Actinobacteria;
       PRINTS; PR00010; EGFBLOOD.
PRINTS; PR00011; EGFLAMININ
PRINTS; PR01452; NOTCH.
                                                                                                                                                                                            Submitted (SEP-2000) to EMBL; AF164486; AAD46653
                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Actinomycetales; Corynebacterineae;
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                    NOTCH 3 PROTEIN
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                                                                       Pfam;
                                                                                                                     InterPro;
                                                                                                                                 InterPro;
                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                      "Rattus norvegicus mRNA
                                                                                                                                                                                                                                 Haritunians T
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
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                                            PF00023; ank; 6.
PF00008; EGF; 34.
PF00066; notch; 3
                                                                                                                                                                                 P00740;
SM00248;
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                                                                                          ; IPR000152; Asx_hydroxyl.
; IPR000561; EGF-like.
; IPR000742; EGF_2.
; IPR001881; EGF_Ca.
; IPR001438; EGF_II.
; IPR002049; Laminin_EGF.
                                                                                 IPR002049;
IPR000800;
                                                                                                                                                                     IPR002110; ANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                   1EDM
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Last sequ
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4; Mismatches
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                                                                                                                                                                                                         EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
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annotation update)
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4.4;
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                                                                                                                                                                                                                                 Schanen N.C.;
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Matches
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                                                                                                                                                  Q9V197 PRELIMINARY;
Q9V197;
01-MAY-2000 (TrEMBLrel. 13, C
01-MAY-2000 (TrEMBLrel. 13, L
01-MAY-2000 (TrEMBLrel. 13, L
CG14604 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00001; EGF_like; 12.
SMART; SM00004; NL; 3.
PROSITE: PSECOCO
                                                              Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    German Neurospora genome project;
Submitted (JUL-2000) to the EMBL/
EMBL; AL389900; CAB97455 1; -
SEQUENCE 217 AA; 23786 MW; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomy
Sordariales; Sordariaceae; Neurospora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15
01-OCT-2000 (TrEMBLrel. 15
01-OCT-2000 (TrEMBLrel. 15
'RELATED TO FINGER PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9P3L0;
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PROSITE; PS50297; ANK_REP_REDON: 1.
PROSITE; PS500207; ASK_HYDROXYL; 1.
EGF-like domain; Glycoprotein; Hydroxylation.
SEQUENCE 2319 AA; 244298 MW; 243BCA02D7C3283D CRC64;
                      Ephydroidea; Drosophilidae; Drosophila NCBI_TaxID=7227;
                                                                                                                                    CG14604
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Nyakatura G., Mewes
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                                                                                                                                                                                                                                                                                                                                                                         109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
21; Conserv
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39.3%;
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2IN XFG 68.
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                                                                                       Hexapoda;
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                                                                   Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fartmann B.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 217;
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                                                                                       Insecta;
                                                                 Muscomorpha;
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RA Beleson K.Y. Benos P.V. Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bottlier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Botshakov S.,
RA Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA de Dodson K., Doup L.E., Downes M., Duyan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Duyan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gubart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gubar P., Harris M.,
RA HOstin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li Z., Liang Y., Lin X.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Spier E., Siden-Kiamos I., Simpson M., Strong R., Sung A.H., Wang X.,
RA Walls S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Shang G., Zhao Q., Zheng L.,
RA Gibbs R.A., Myers E.W., Zhong W., Zhon W., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Zhong W., Zhou S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Zhong W., Zhou S., Zhu X., Smith H.O.,
RA Glode C. 287:2195-2195 (2000).
DR EMBL, Aeddord C.C. Adedo.
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Best Local S
Matches 21
            D Q9L1C8 PRELIMINARY; PRT; 1212 AA.

C Q9L1C8;
C Q9L1C8
T 01-OCT-2000 (TrEMBLrel. 15, Created)
T 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
T 01-UN-2001 (TrEMBLrel. 17, Last annotation update)
E PUTATIVE NITROREDUCTASE.
N SCL11.10C.
Streptomyces coelicolor.
C Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
C Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycetales; NCBL_TaxID-1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     George R.A., Lewis S.E., Richards S., Ashburner M., Hend
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., P.
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Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adams M.D., Celniker S.E., Holt R.A., Ev Amanatides P.G., Scherer S.E., Li P.W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                   121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRPAAVP----VPLRMQPGPAHPVLS-----FLRPSWDLVSAFYSLPLAPLSPT
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                                                                                                                                                                                                                                                                                                                                                                          59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 77.5; DB Pred. No. 3.1; 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23;
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                                        Streptomyces
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Galle R.F.,
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Baldwin D.,
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 12.5 KDA PROTEIN (ORF-3).
Swine hepatitis E virus.
Viruses; ssRNA positive-strand viruses, no DNA stage.
                                                                                                                                                                                                                                                                                                                                                                                               036612;
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InterPro; IPR003415; Nitroreductase.
InterPro; IPR002965; P_rich_extensn.
Pfam; PF02277; DBI_PRT; 1.
Pfam; PF00881; Nitroreductase; 1.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR01217; PRICHEXTENSN.
E898B903F78D235A CRC64;
                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 94:9860-9865(1997).
EMBL; AF082843; AAC97209.1; -
InterPro; IPR003384; HEV_ORF2.
Pfam; PF02444; HEV_ORF2; 1.
SEQUENCE 122 AA; 12466 MW; 77602F9048E7B12A C
                                                                                                                                                                                                   "A novel virus in swine is closely related to the human virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-A3(2);
Oliver K., Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "A set of ordered cosmids and a detailed genetic and physical map for the 8 mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
EMBL; AL157953; CAB76073.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-97000351; PubMed-8843436; Redenbach M., Kieser H.M., Denapaite D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-A3(2);
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oliver K., Harris D.; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                              MEDLINE=97420774; PubMed=9275216;
Meng X.J., Purcell R.H., Halbur P.G., Lehman J.R., Webb D.M.,
Tsareva T.S., Haynes J.S., Thacker B.J., Emerson S.U.;
                                                                                                                                                                                                                                                                  STRAIN-MENG
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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58
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                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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36.7%;
                                                                                      18.4%;
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Pred. No. 8;
7; Mismatches
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                                                                                      Score 77;
Pred. No.
                                                                                                                                         77602F9048E7B12A CRC64;
                                                                          Mismatches
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                                                                                     DB 12; Length 122; 0.85;
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Search completed: April 11, 2002, 09:35:06 Job time: 323 sec



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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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US-08-340-428B-49
US-08-468-57B-12
US-08-468-577B-12
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US-08-615-170-21
US-08-615-170-21
US-08-615-170-19
US-09-461-697-54
US-09-461-697-54
US-09-461-697-52
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US-08-471-971-3
US-08-489-3
US-08-471-971-3
PCT-US93-08849-3
US-08-240-049B-19
US-08-240-049B-19
US-08-471-93-21
US-08-471-293-21
US-08-471-293-21
US-08-818-112-143
US-08-760-489-4
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Compugen
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87.704 Million cell updates/sec
                       Sequence 49, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 21, Appl
Sequence 54, Appl
Sequence 58, Appl
Sequence 54, Appl
Sequence 54, Appl
Sequence 54, Appl
Sequence 57, Appl
Sequence 58, Appl
Sequence 59, Appl
Sequence 3, Appl
Sequence 21, Appl
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                        ; SEQUENCE CHARACTERISTICS:
; LENGTH: 1257 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-340-428B-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-340-428B-49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 49, Applicat Patent No. 5648465
GENERAL INFORMATION:
                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,428B
FILING DATE: 14 No. 5648465ember 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/922,911
FILING DATE: 03 August 1992
CLASSIFICATION: 514
APTORNEY/ACENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REGISTRATION NUMBER: Margolis=1A
TELECOMMUNICATION INFORMATION:
TELEPAX: 202-628-5197
TELEPAX: 202-628-5197
Query Match
Best Local Similarity
                                                                                                                                                             TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: CLONING, TITLE OF INVENTION: NEUROCAN NUMBER OF SEQUENCES: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: RAUCH, UWE APPLICANT: MARGOLIS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MARGOLIS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Browdy
STREET: 419 Sevent
CITY: Washington-
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RAUCH, Uwe
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US-08-525-864A-2
US-09-041-886-25
PCT-US94-05277-2
US-09-220-641-3
US-08-818-112-142
US-09-150-460B-10
US-09-220-641-5
US-08-240-049B-20
US-08-4477-292-22
PCT-US95-137703-22
US-08-469-412A-7
US-08-469-412A-7
US-08-469-412A-2
US-08-469-412A-2
US-08-469-112A-2
US-08-252-966B-12
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Result No.

Score

Match

Length

DB

Query

Pred. No. is the nu score greater than and is derived by a

Minimum DB Maximum DB

seq

length:

0

length: 2000000000

Minimum

Title: Perfect score:

US-09-234-208B-1

Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 ,

Gapext 0.5

212252 seqs,

Database

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2.
2: /cgn2_6/ptodata/2.
3: /cgn2_6/ptodata/2.

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US-08-468-576B-12; Sequence 12, Application US/08468576B; Patent No. 5955345; GENERAL INFORMATION:
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                                                                                                                                                                Matches
                                                                                                                                                                                          Query Match
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APPLICANT: Uhl, G
                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 236687
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                             FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            670 SVPEEQAVRPVSFG-AEDPE 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     610 SSIPSEALSAVSLQASPGDGSPDFPIVAMLRAPKLWLLPHSTLVPNVSPIPLSPASPLPS 669
                                                                                                                                                               Local Similarity
nes 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 0646/1A843-US5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 33,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 28-APF
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                                                                                                     32 TASPSPAPSWTPSP---RPGPAHP---FLQPPWAV--ALWSL 65
                                                                                                                                                                                                                                                                                  ORGANISM:
                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                      2 THSLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSL 43
                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
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                                                                                                                                                                                                                                                                                                                                                     : 440 amino acids amino acid
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Wang, Jai-Bel
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                             N-terminal
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45.2%;
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                                                                                                                                                                              Score 72; D
Pred. No. 1;
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US-08-468-579B-12
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                                                                             Sequence 12, Application US/08468579B Patent No. 5981700 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (914) 332-18 INFORMATION FOR SEQ ID NO:
            APPLICANT: Rabin, Dar
TITLE OF INVENTION: F
TITLE OF INVENTION: C
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: MI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
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PRIOR APPLICATION UMBER: US 07/312,543
FILING DATE: 17-FEB-1989
ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: System
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: OB
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                           480 ILSSLN 485
                                                                                                                                                                                                                                                                              421 AAQPLNLSSRPKTAEPVKSPTSPTQNLFPASKTSPVNLPNKSSIP-SPIGGSLGRGSSLD 479
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                                                                                                                                                                                                                                           68 AHVAVN 73
                                                                                                                                                                                                                                                                                                              10 AAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPV--SVGRGPDPD 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
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660 White Plains Road
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                                                                   Rabin, Daniel
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04-DEC-1989
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08-JUN-1992
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14-JUN-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UMBER: US/08/468,576B
O6-JUN-1995
                PANCREATIC ISLET CELL ANTIGENS OBTAINED BY MOLECULAR CLONING: 19
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                                                                                                                                                                                                                                                                                                                                                               17.1%; Score 71.5; 34.8%; Pred. No. 1.
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STREET: 000 CITY: Tarrytown CTATE: New York

ADDRESSEE: Sprung Kramer Schaefer & Briscoe STREET: 660 White Plains Road

COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,

3.50 inch,

1.4 Mb storage

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Matches 23; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local !
                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Rabin, Daniel
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INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: US 07
FILING DATE: 17-FEB-1989
'ATTORNEY/AGENT INFORMATION:
STREET: OUU
STREET: NEW YORK
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/715,181
                                                                                                                   TITLE OF INVENTION: PANCREATIC ISLET CELL ANTIGENS TITLE OF INVENTION: OBTAINED BY MOLECULAR CLONING
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PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
                                                                                NUMBER OF SEQUENCES: 1
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                             68 AHVAVN 73
                                                                                                                                                                                                                                                                                                                                                                                      10 AAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPV--SVGRGPDPD 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/441,703 FILING DATE: 04-DEC-1989
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OPERATING SYSTEM: System
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                                                                ADDRESSEE:
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                                                2E: Sprung Kramer Schaefer & Briscoe
660 White Plains Road
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17-FEB-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                               13; Mismatches
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                            CORRESPONDENCE ADDRESS:
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REFERENCE/DOCKET NUMBER: MDI
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                  NUMBER OF SEQUENCES:
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                                                                                          CITY: Los Angeles
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 AAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPV--SVGRGPDPD 67
                                                                       COUNTRY:
                                                                                                                            STREET:
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                                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQPLNLSSRPKTAEPVKSPTSPTQNLFPASKTSPVNLPNKSSIP-SPIGGSLGRGSSLD 479
                                                          9007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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                                                                                                                           E: Pretty, Schroeder, Brueggemann & Clark 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   604 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (914) 332-1844
                                                                         USA
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                                                                                                                                                                                               ASSAYS FOR THE IDENTIFICATION OF CAMP AND MITOGEN COMPOUNDS WHICH INHIBIT ACTIVATION OF CAMP AND MITOGEN RESPONSIVE GENES
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                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: MONTMINY, Marc R.
APPLICANT: MONTMINY, Marc R.
TITLE OF INVENTION: Methods for Treating Diabetes
FILE REFERENCE: SALK1650-1
CURRENT FILING DATE: 1997-10-31
EARLIER APPLICATION NUMBER: US 194,468
EARLIER FILING DATE: 1994-02-10
                                                                                                                                    Matches
                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08961739A
Patent No. 6063583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity Matches 23; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 4
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                                                                                                                                                                                                                                   NAME/KEY: VARIANT
LOCATION: (1)...(2441)
OTHER INFORMATION: Xaa = Any Amino Acid
                                                                                                                                                                                                                                                                                                        ORGANISM: Mus
                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                          ENGTH: 2441
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REFERENCE/DOCKET NUMBER: P41 9672
TELECOMMUNICATION INFORMATION:
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LENGTH: 2441 amino aci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  900 PTP 902
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900 PTP 902
                                                                 843 SQLPCPPVTQSPLHPTPPPASTAAGM--PSLQHPTAPGMTPPQPAAPTQ-PSTPVSSGQT 899
                                                                                                                        17.18;
Local Similarity 36.58;
les 23; Conservative
                                 64 PDP 66
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SOFTWARE: Patenti
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                                                                                               4 SLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSVGRG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 SLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPISPVSVGRG 63
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(619)-546-9392
TD NO: 2:
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n Release #1.0, Version #1.25
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Pred. No. 10;
                                                                                                                                                  Score 71.5;
Pred. No. 10;
                                                                                                                                Mismatches
                                                                                                                                                                  DB 3;
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                                                                                                                                                                  Length 2441;
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US-08-615-170-19

US-08-615-170-19

; Sequence 19, Application US/08615170

· Patent No. 5776776
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GENERAL INFORMATION:
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                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein 1-615-170-21
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/191,493
FILING DATE: 04-FEB-1994
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APPLICATION NUMBER: 1
FILING DATE: 06-FEB-
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                         155 SAAPRFWSGPIP--GQPGPSQDIKPFAQPAYPIQPPMPPSLASYE-PLAPLPPAASAVPV 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
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STATE: California
                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                              4 SLLPRPAAVPVPLRMQPGPAHPVLSFLRPSWDLVS-----AFYSLPLAPLSP--TSVPI 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94105-1493
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5776776
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                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         (415) 326-2400
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326-2422
30; 21;
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                                                                                                                                                                                              16.6%; Score 69.5; | 35.0%; Pred. No. 2; tive 11; Mismatches
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GENERAL INFORMATION:

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APPLICANT:
APPLICANT:

ORDAHL, Charles P. AZAKIE, Anthony MAR, Janet H.

APPLICANT:

FARRANCE, Iain K.G

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GENERAL INFORMATION:

APPLICANT: COGENT NEUROSCIENCE, Inc.

APPLICANT: Lo, Donald C.

APPLICANT: Lo, Donald C.

APPLICANT: Barney, Shawn

APPLICANT: Thomas, Mary Beth

APPLICANT: Portbury, Stuart D.

APPLICANT: Fouranam, Kasturi

APPLICANT: Katz, Lawrence C.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING

TITLE OF INVENTION: CELL DEATH

FILE REFERENCE: 10001-005-999
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; Sequence 58, Application US/09461697
; Patent No. 6277974
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CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
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INFORMATION FOR SEQ ID NO: 19:
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REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
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ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
US 08/191,493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01526
FILING DATE: 06-FEB-1995
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                           156 SAAPRFWSGPIP--GQPGPSQDIKPFAQPAYPIQPPMPPSLASYE-PLAPLPPAASAVPV 212
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TYPE: a
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STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity es 21; Conserv
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STEWART, Alexandre F.R.
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35.0%;
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Pred. No. 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens US-09-461-697-54
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                                                                                                                                                                US-09-461-697-52
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                                                                                                               GENERAL INFORMATION:
                                                                                                                            Sequence 52, Application US/09461697 Patent No. 6277974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 54
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                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local (
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Best Local (
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                                     APPLICANT: COGENT NEUROSCIENCE,
APPLICANT: Lo, Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: COMPOSITIONS AND METHODS TITLE OF INVENTION: AND TREATING CONDITIONS; TITLE OF INVENTION: CELL DEATH FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 466 SOFTWARE: FastSEQ for Windows Version 4.0
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 132
TYPE: PRT
                                                                                                                                                                                                                                    88 ALTITSLPPGLLPFVGVELTAHPQALIGRG 117
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nes 25; Conserv
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25; Conserv
Portbury, stari
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Thomas, Mary Beth
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27.8%;
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27.88;
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Pred. No. 0
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Pred. No. 0.59;
9; Mismatches 29;
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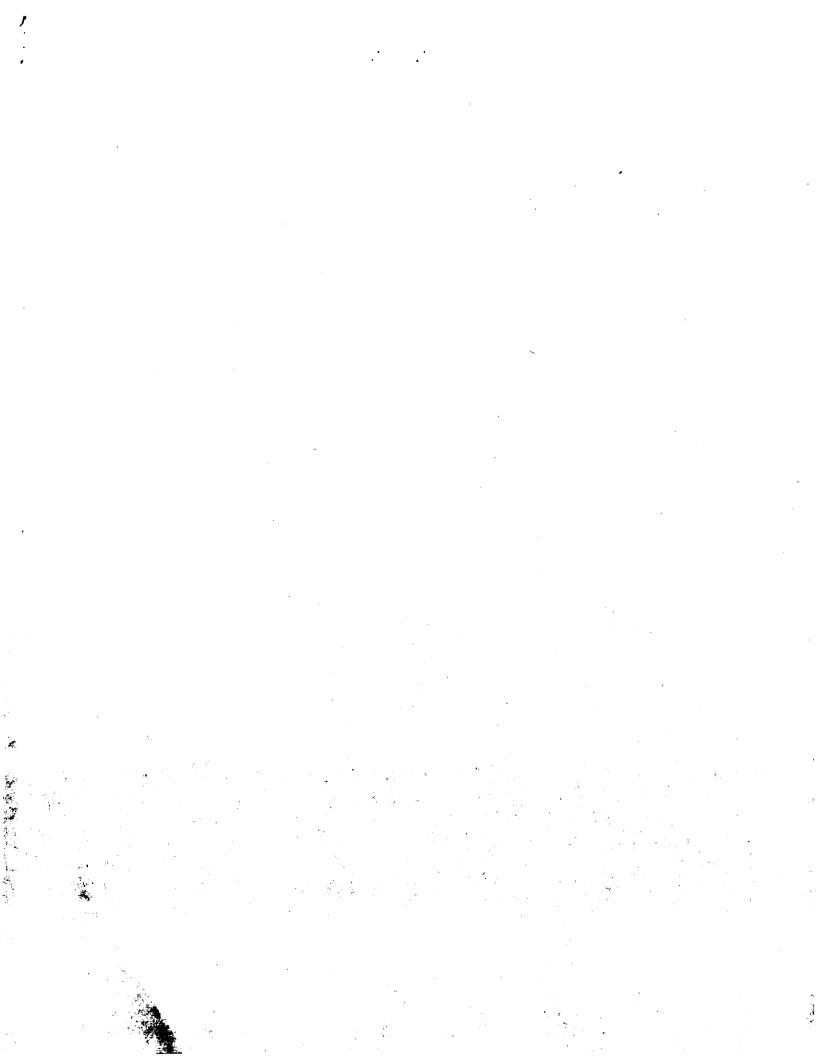
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RESULT 14
US-08-840-316-3
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Sequence 3, Application US/08840316 Patent No. 6054567
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SEQ ID NO 52
LENGTH: 139
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 48
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                                                                                                                                                                                                                                                                                                                    Query Match
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
CURRENT FILING DATE: 1999-12-14
NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING TITLE OF INVENTION: CELL DEATH
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APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
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APPLICANT: Katz, Lawrence C.
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                                                                                                                  115 ALTITSLPPGLLPFVGVELTAHPQALIGRG
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Pred. No. 0.74;
9; Mismatches 29;
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Best Local S
Matches 23
                                                                                                                                                                                                           Sequence 9, Applica
Patent No. 6120988
GENERAL INFORMATION
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASCOPION OF THE PRIOR APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 751-684
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
                                               CORRESPONDENCE ADDRESS
                                                                             TITLE OF INVENTION:
                                                                                                            APPLICANT: Tam, Albert APPLICANT: Fry, Kirk E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Richard W. Bork
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                107 APPLPHV 113
ADDRESSEE: Dehlinger - compress: 350 Cambridge Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                48 AAVPAVVSGVTGLILSPSQSPIFIQPTPS-PPMSPLRPGLDLVFANPPDHSAPLGVTRPS 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: unl
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                52 SVPISPV 58
                                                                                                                                                                                                                                                                                                                                                                                                                              10 AAVPV----
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                                                                                                                                                                                                                INFORMATION:
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                                                                                                                                            Reyes, Gregory R
Yarbough, Patrice O
Bradley, Daniel W
Krawczynski, Krzysztof
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM PC COMPATIBLE
                            Dehlinger & Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (212) 758-4800
212) 751-6849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sergei. A., and Robinson, Robin A.
Recombinant Proteins Of
A Pakistani Strain Of Hepatitis E And Their
                                                              DNA Sequences of Enterically Transmitted No. 6120988-A/No..6120988-B Hepatitis Viral Agent 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.1%;
34.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use In Diagnostic Methods And Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                             ----PLRMQPGPAHPVLSFLRPSWDLVSA---FYSLPLAPLSPT 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 67.5; DB 3; Length 123; Pred. No. 0.71; 8; Mismatches 17; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2026-4255
                Suite 250
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Search completed: April 11, 2002, 09:29:35 Job time: 72 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-478-507-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/478,507
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/279,823
FILING DATE: 25-JUL-1994
PRIOR APPLICATION NUMBER: US 07/681,078
FILING DATE: 25-JUL-1994
PRIOR APPLICATION NUMBER: US 07/681,078
FILING DATE: 05-APR-1991
PRIOR APPLICATION NUMBER: US 07/505,888
FILING DATE: 05-APR-1990
PRIOR APPLICATION NUMBER: US 07/420,921
FILING DATE: 13-OCT-1989
PRIOR APPLICATION NUMBER: US 07/467,486
FILING DATE: 16-JUN-1989
PRIOR APPLICATION NUMBER: US 07/367,486
FILING DATE: 11-APR-1989
PRIOR APPLICATION NUMBER: US 07/36,672
FILING DATE: 11-APR-1989
PRIOR APPLICATION NUMBER: US 07/36,672
FILING DATE: 11-APR-1989
PRIOR APPLICATION NUMBER: US 07/36,672
FILING DATE: 11-APR-1989
PRIOR APPLICATION NUMBER: US 07/208,997
FILING DATE: 11-APR-1989
PRIOR APPLICATION NUMBER: 4600-0183.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0880
TELEPHONE: (650) 324-0860
INFORMATION FOR SEG ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                         Query Match 16.1
Best Local Similarity 34.3
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                 107 APPLPHV 113
                                                                                                                                                               52 SVPISPV 58
                                                                                                                                                                                                                                       CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                              48 AAVPAVVSGVTGLILSPSQSPIFIQPTPS-PPMSPLRPGLDLVFANPPDHSAPLGVTRPS 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                    16.1%; Score 67.5; DB 3; Length 123; 34.3%; Pred. No. 0.71; rative 8; Mismatches 17; Indels 19
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Result
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Maximum DB seq
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                                                        No
                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
        Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      length: 0
length: 2000000000
                                                                                                                                                                                                                                                      Match
        Query
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                            1: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT: *
2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT: *
3: SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT: *
4: /SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT: *
5: /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT: *
5: /SIDS8/gcgdata/geneseq/geneseqp/AA1984.DAT: *
6: /SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT: *
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16: /SIDS8/gcgdata/geneseq/geneseqp/AA1995.DAT: *
17: /SIDS8/gcgdata/geneseq/geneseqp/AA1996.DAT: *
18: /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT: *
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19: /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT: *
20: /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT: *
21: /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT: *
22: /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT: *
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2287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              522463 segs, 74073290 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MELAALCRWGLLLALLPPGA.....VGRGPDPDAHVAVNLSRYEG
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                                                                                                                                                                                                                                                      Length
                                            919
1200
1255
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    AAY97240
AAB60408
AAB61593
AAB21200
AAB21204
AAW19764
AAW12708
AAB21203
AAB21203
AAW01111
AAW92406
AAB21198
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                                                                                                                                                                                                                                                                                                               SUMMARIES
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Extracellular HER-Human HER-2/neu fu Her2-CM-CSF immuno Human HER-2/neu fu Human HER-2/neu protein.
Human HER-2/neu on Human HER-2/neu on Human HER-2/neu protein.
                                                                                                                                                                                                                                                 Description
                                                                                                                                                              Truncated HER-2, p
Human ErbB2 oncopr
Human ErbB2 extrac
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342 17			1308 1		œ				910 1									166 1										_	N	5 2	55 2	55 2	1255 2
										1 AAY67309							2 AAB62074						1 AAB21206		1 AAB21205						AAB8	. AAYS	1 AAY8478
53	33	99	ω ω	41	23	25	34	43	37	9	20	16	59	9	37	63	74	45	67	72	54	60	90	99	05	22	93	88	67	67	58	20	80
erbB-3 polypeptide	EGF receptor relat	Human indu	Receptor tyrosine	HER4. Home	Human epid	Human epidermal	Receptor tyrosine	HER4 with alternat	HER4-Ig fu	Epidermal growth	Amino acid sequenc	Human EGF	Amino acid sequenc	LD1D2D3.Apal EGF	Epidermal growth	Human ErbB2	ErbB2 prot		_		Human ErbB2		Ō		Rat HER-2/neu	Extracellular	DC8scFv-erbB2EC	Sequence of c-erbs		=	Human HER-		Amino acid
ypeptide	or relat	inducible ni	yrosine	_		ermal gr	yrosine	alternat	sion pro	growth f	sequenc	receptor	sequenc	al EGF r	growth f	2 extrac	—			recep	2 protei	acid sequenc	Her-2/neu pr	neu prot	neu prot	ď	bB2EC fu	f c-erbB	Į.	O)	HER-2/neu pr	മ	sequenc

ALIGNMENTS

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RESULT
AAY97240
 FT FT TT
                           /note=
Misc-difference 359
                                                                    /note= "Preferably Pro" Misc-difference 347
                                                                                         /note= "Preferably Ser" Misc-difference 346
                                                                                                            /note= "represented as Agn" Misc-difference 343
                                                                                                                                                Location/Qualifiers
                                              /note=
Misc-difference 357
                                                                                                                                                                                                     HER-2; erbB-2; oncogene; receptor-like tyrosine kinase; insertion; extracellular domain IIIa; antagonist; intron 8; C-terminal extension; truncated HER-2; p68; dimerization inhibitor; cytostatic.
Misc-difference
                 Misc-difference
                                                                                                                                     Misc-difference 125
                                                                                                                                                                                                                                                Truncated HER-2, p68-HER-2.
                                                                                                                                                                                                                                                                   04-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                                         AAY97240 standard; protein;
                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                       AAY97240
/note=
377
                 /note= "Preferably Leu"
362
                                                                                                                                             note= "represented as Agn"
                                                                "Preferably Leu"
       "changes from glycine"
                                              "Preferably Gln"
                                                                                                                                                                                                                                                                                                           420
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HER-2/neu (erbB-2) oncogene encodes a receptor-like tyrosine kinase. The extracellular domain of p185-HER-2 is proteolytically shed from breast carcinoma cells in culture and is found in serum of some cancer patients and may be a serum marker of metastatic breast cancer. An alternative HER-2 mRNA of 4.8 kb with a 274 bp insert (intron 8) has been identified. The retained intron is in-frame and encodes a 79 amino acid extension designated ECDIIIa (the present sequence), which is inserted at residue 340 of p185-HER-2. The alternative mRNA predicts a truncated HER-2 protein (approximately 68 kba) that lacks the transmembrane and intracellular domains (see Ax97240). p68HER-2 specifically binds to p185-HER-2 without activating HER-2. It could therefore block dinerization of p185-HER-2. The p66HER-2 polypeptide binds to a site on the ECD of HER-2 that is different from the site of binding for Herceptin (RTM) (a marketed humanized monoclonal antibody that is used for the treatment of cancer and binds to the ECD of HER-2). The methods, compositions, polypeptides and antibodies are used to treat solid candyor colon cancer, especially where over-expression of HER-2 is
                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Using polypeptides and antibodies that bind to the extracellular domain of the receptor-like tyrosine kinase HER-2 to treat solid tumors of the breast, lung, ovaries and colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; Page 39-40; 46pp; English.
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241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
                                                                                                                                                                                                                                                                                                                                          AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
                                           LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
                                                                                                                                         DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
                                                                                                                                                                                                                                         eltylptnaslsflqdiqevqgyvlcahnqvrqvplqrlrivrgtqlfednyalavldng
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395
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414
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                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 2158.5; DB 2
Pred. No. 2.1e-166;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21; Length 420;
                                                                                                                                                                                                                                                                                                                                                                                                                                             19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 light chain variable region; cancer; cytostatic; EGFR-expressing cancer; epidermal growth factor receptor; colon cancer; rectal cancer; tumour; colorectal cancer; non-small cell lung cancer; metastatic breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-ErbB2 monoclonal antibody 2C4; HER2; mouse; murine; humanised; VL; light chain variable region; cancer; cytostatic; EGFR-expressing cancer epidermal growth factor receptor; colon cancer; rectal cancer; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB60408;
                                                                                                                                                                                                                                                                                                 Treating cancer in a hun factor receptor (EGFR),
                                                                                                                                                                                                                                                                                                                                 WPI; 2001-080862/09
                                                                                                                                                                                                                                                                                                                                                                                                                    23-JUN-2000; 2000WO-US17366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      affinity purification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human ErbB2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-APR-2001
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                                                                                                                                                                                                                                                                    Example
                                                                                                                                                                                                                                                                                                                                                        Adams CW,
                                                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH
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                                                                                                                                                                                                                                                                    1; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; Protein;
                                                                                                                                                                                                                                                                                                                                                      Presta LG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oncoprotein, SEQ
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                                                                                                                                                                                                                                                                                                   human, where
R), comprises
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                                                                                                                                                                                                                                                                                                   the cancer expresses epidermal growth administering an antibody which binds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer;
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especially colon cancer, rectal cancer, colorectal cancer, lung cancer (especially non-small cell lung cancer), or breast cancer (especially metastatic breast cancer). The antibodies may also have non-therapeutic uses e.g., as affinity purification agents. Using an antibody which binds to ErbB2 to treat cancer is preferable to the use of EGFR-targetted drugs, as EGFR is also highly expressed in other tissues such as the liver and skin, where the active drug will also bind, with skin toxicity having been observed for EGFR-targetted drugs. Antibodies which bind ErbB2 are anticipated to have a better safety profile than such drugs. The invention relates to a method for treating cancer in a human patient wherein the cancer expresses epidermal growth factor receptor (EGFR), comprising administering an antibody which binds ErbB2 (HER2; AAB60408). act by antagonising ErbB receptors, and as inhibitors of transforming growth factor alpha (TGF-alpha)-activated mitogen activated protein kinase (MAPK). The method of the invention is used for treating cancer, comprising such nucleic acids; the recombinant production of a humanised ErbB2-binding antibody; and an immunoconjugate comprising a humanised ErbB2-binding antibody and a cytotoxic drug. The ErbB2-binding antibodies In particular, the anti-ErbB2 antibody is the murine monoclonal antibody 2C4 (AAB60396, AAB60399) or a humanised version of 2C4 (AAB60398, AAB60399). The invention also encompasses an isolated nucleic acid encoding a humanised ErbB2-binding antibody; vectors and host cells present sequence represents human cancer in a human patient,

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                                                                  (GETH )
       Treating prostate cancer in a human comprises administering an antibody which binds ErbB2 and blocks ligand activation of an ErbB receptor -
                                  WPI; 2001-159131/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                            25-JUN-1999;
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                                                                                                                               04-JAN-2001.
                                                                                                                                               WO200100238-A1
                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                antibody; ErbB
                                                                                                                                                                                                           Human
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                                                                                                                                                                                                          ErbB2 extracellular domain.
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                                                                   GENENTECH INC.
SLOAN KETTERING INST CANCER
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                                                                                                              2000WO-US17423
                                                                                                                                                                               cytostatic; prostate cancer; receptor tyrosine kinase; B receptor; monoclonal antibody 2C4; variable light cha
                                                                                            99US-0141315
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83.0%;
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Pred. No. 1.7e-143;
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                                                                                       HER-2/neu; oncogene; tyrosine kinase;
breast cancer; prostate cancer; ovari
                                                                                                                                                                     AAB21200;
                                                                                                                                                                                           AAB21200 standard; protein;
                                WO200044899-A1
                                                                                                                        Extracellular HER-2/neu protein.
                                                                                                                                              12-JAN-2001
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Pred. No. 1.7e-143;
9; Mismatches 45;
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                                                                                                cytostatic;
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Best Local S
Matches 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CORI-)
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SMITHKLINE BEECHAM
          standard;
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83.0%;
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Pred. No. 1.7e-143;
9; Mismatches 45;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                The present sequence is a fusion protein comprising the extracellular domain and a preferred portion of the phosphorylation domain of the hum HER-2/neu protein. HER-2/neu is a member of the tyrosine kinase family receptor-like glycoproteins and shows homology to the epidermal growth factor receptor (EGFR). It probably plays a part in cell growth and/or differentiation. The HER-2/neu gene is an oncogene. HER-2/neu fusion proteins may be used to treat or prevent cancer by eliciting or enhanci an immune response to the HER-2/neu protein. They may be used to treat malignancies such as breast, ovarian, colon, lung and prostate cancers, and may be used as an antigen to vaccinate against these neoplasias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 27;
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breast cancer; prostate cancer;
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                                    AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
 YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCAR---
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te cancers -
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SMITHKLINE BEECHAM
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83.0%;
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cer; ovarian cancer; lung can
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Pred. No. 1.9e-143;
9; Mismatches 45;
 -GTHSLLPRPAAVPVP
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                              that is overexpressed in breast, ovarian can other cancer cells, and granulocyte-macrophage colony stimulating factor (GM-CSF). It is the expression product of a nucleic acid molecule (AAT72725) prepd. by PCR amplification of Her2 cDNA from a breast cancer cells line and fusion to GM-CSF cDNA. Fusion expression vectors can be used to transfect mammalian and insect cells. The Her2-GM-CSF fusion protein is used to generate anti-Her2 immunity. Tumour cells are eliminated by cytotoxic T lymphocytes activated in vivo or in vitro by exposure to antigen-presenting cells exposed to the
Sequence
                                                                                                                                      A fusion protein (AAW19764) comprises Her2 (a growth factor receptor
                                                                                                                                                               Disclosure; Fig 8; 45pp; English
                                                                                                                                                                                       vertebrate
                                                                                                                                                                                              Potent APC that activates T-cells to give multivalent cellular immune response - can also induce a cytotoxic T-cell response in
                                                                                                                                                                                                                                     N-PSDB;
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Query Match

82.1%;

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Claim 2; Fig 12; 128pp; English
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                                                                         HER-2/neu extracellular domain/phosphorylation domain fusion proteins useful for vaccinating against breast, ovarian, colon, lung and
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breast cancer; prostate cancer; ovarian cancer; lung cancer;
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cches 45;
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RESULT
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ID AAB2
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Best Local Similarity
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28-JAN-2000; 2000WO-US02164.
                                  03-AUG-2000
                                                                   WO200044899-A1
                                                                                                                                                       Human; HER-2/neu; oncogene; tyrosine kinase;
breast cancer; prostate cancer; ovarian cance
                                                                                                                                                                                                              Human
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                                                                                                                                         cancer.
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Pred. No. 2.7e-143;
9; Mismatches 45;
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                                                                                                                                                       nase; cytostatic; vaccine;
cancer; lung cancer;
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Best Local S
Matches 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      {\rm HER}\text{-}2/{\rm neu} extracellular domain/phosphorylation domain fusion proteins useful for vaccinating against breast, ovarian, colon, lung and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                              DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
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DB; AAA89736.
                         --PDAHVAVNLSRYEG
                                                              LRMQPG--PAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPTI------SPVSVGRGPD 405
                                                                                                                   YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCAR-----GTHSLLPRPAAVPVP
                                                                                                                                                          aagctgpkhsdclaclhfnhsgicelhcpalvtyntdtfesmpnpegrytfgascvtacp
                                                  iqefagckkifgslaflpesfdgdpasnt---aplqpeqlqvfetleeitgylyisawpd
                                                                                                      ynylstdvgsctlvcplhnqevtaedgtqrcekcskpcarvcyglgmehlrevravtsan
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83.0%;
433
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1878; DB 21;
Pred. No. 3.8e-143;
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Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                which the oncogene is associated. The polypeptide can be produced in transformed host cells for use in immunisation. Alternatively, animal cells are transfected in vivo or ex vivo with a viral vector that directs expression of the polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Page 56-61; 71pp; English
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DB; AAT40739.
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83.0%;
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Pred. No. 4e-1
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4e-143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HER-2/neu oncogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              used for prevention
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Query Match Best Local Matches

Similarity

82.1%;

Score 1878; DB 2 Pred. No. 4e-143; Mismatches

DB 20;

Length Indels

20;

Gaps

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Conservative

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RESULT 1
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                                                                                                                                                                                                                                                         01-APR-1996;
17-MAR-1993;
12-AUG-1993;
31-MAR-1995;
                   This sequence represents the human HER-2/neu oncogene protein. A fragment of this protein is used in a method for eliciting or enhancing an immune response to HER-2/neu protein. The polypeptide can stimulate T cells and B cells to produce an immune response to the HER-2/neu protein. The method can be used for immunisation against a malignancy in which the HER-2/neu oncogene is associated and in the treatment of an existing tumour, or to prevent tumour occurrence or reoccurrence.
                                                                                                                              Use of HER-2/neu polypeptides - for an HER-2/neu associated malignancy, preventing tumours
                                                                                                          Claim 3; Column 31-38; 26pp; English.
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                                                                                                                                                                                                                                                                                                                                      09-FEB-1999
                                                                                                                                                                                                                                                                                                                                                            US5869445-A
                                                                                                                                                                                                                                                                                                                                                                                                        Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                  malignancy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             HER-2/neu; oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human HER-2/neu oncogene protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-APR-1999
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Sequence
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DB; AAX01912.
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                                                                                                                                                                                                              MA,
 1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                   treatment;
                                                                                                                                                                                                              Disis ML;
                                                                                                                                                                                                                                   WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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93US-0033644.
93US-0106112.
95US-0414417.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             immune response;
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  В
                                                                                                                                                                                                                                                                 Human; HER-2/neu; oncogene; tyrosine kinase; cyt
breast cancer; prostate cancer; ovarian cancer;
                                                                                                                                                                                  28-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                    AAB21198 standard; protein;
                              Claim
                                                prostate
                                                       HER-2/neu extracellular domain/phosphorylation domain fusion proteins useful for vaccinating against breast, ovarian, colon, lung and
                                                                                                                                                               29-JAN-1999;
                                                                                                                                                                                                    03-AUG-2000
                                                                                                                                                                                                                      WO200044899-A1
                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                              Human HER-2/neu protein.
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present sequence is the human HER-2/neu tyrosine kinase family of receptor-like
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DB; AAA89736.
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                                                                                                                                                                                                                                                                                                                                                                                                                    --PDAHVAVNLSRYEG
                                                                                                                                                                                                                                                                                                                                                                                                                                        iqefagckkifgslaflpesfdgdpasnt---aplqpeqlqvfetleeitgylyisawpd 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ynylstdvgsctlvcplhnqevtaedgtqrcekcskpcarvcyglgmehlrevravtsan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
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                             52; Fig 7; 128pp; English.
                                                                                                                                                                                                                                                          cancer.
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                                                                                                                                  CORIXA CORP.
SMITHKLINE BEECHAM
                                                                                                               Gheysen
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                                                                                                                                                                                                                                                                                                                 (first entry)
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protein. It is a r
glycoproteins and
                                                                                                                                                                                                                                                                           cytostatic; vaccine;
                                                                                                                                                                                                                                                                   lung cancer;
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01-OCT-1999;

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RESULT 1
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Best Local S
Matches 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homology to the epidermal growth factor receptor (EGFR). It probably plays a part in cell growth and/or differentiation. The HER-2/neu gene is an oncogene. An HER-2/neu fusion protein comprising a HER-2/neu extracellular domain fused to a HER-2/neu phosphorylation domain may be used to treat or prevent cancer by eliciting or enhancing an immune response to the HER-2/neu protein. It may be used to treat malignancies such as breast, ovarian, colon, lung and prostate cancers, and may be used as an antigen to vaccinate against the content of the prostate cancers.
                                                                                                                                         SPLICE erbB-2 receptor protein; cell transformation disorder;
                                                                                                                                                                                             08-AUG-2000
                                                                                                                                                                                                                                           AAY84780 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                   13-APR-2000.
                                                                                Homo sapiens
                                                                                                         wound
                                                                                                                                tumor cell proliferation; tissue
                                                                                                                                                                   Amino acid sequence of the SPLICE erbB-2 receptor protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
                                                                                                                      resorption;
                                                                                                                                                                                                                                                                                                                                                 iqefagckkifgslaflpesfdgdpasnt---aplqpeqlqvfetleeitgylyisawpd
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362; Conservative
                                                                                                        healing.
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83.0%;
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Pred. No. 4e-143;
9; Mismatches 45;
                                                                                                                      disease;
                                                                                                                                   degeneration;
                                                                                                                     degenerative
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a SPLICE erbB-2 receptor protein. The protein has an in-frame deletion of 16 amino acids, 2 of which are conserved cysteine residues, compared to the unspliced protein. The erbB-2 polynucleotide is used to construct probes for detecting disorders of cell transformation such as cancer. Antibodies to the protein may be used to detect SPLICE erbB-2 in a sample. Agents (e.g. antisense oligonucleotides) which inhibit the expression of SPLICE erbB-2 are useful for reducing tumor cell proliferation and treating cancer. Substances which stimulate SPLICE erbB-2 are useful for treating conditions involving damaged cells including conditions in which degeneration of tissue occurs, such as arthropathy, bone resorption, inflammatory diseases, degenerative disorders of the
  AAY92620;
                     AAY92620 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid encoding an erbB 2 receptor protein designated SPLICE erbB-2, inhibitors of the protein are useful for treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             central nervous system and wound healing
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                                                                                                                                                         AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
                                                                                                                                                                                                                                                       LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
                                                                                                                                                                                                                                                                                    ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
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DB; AAA14812.
                                                                                              --PDAHVAVNLSRYEG
                                                                                                                 iqefagckkifgslaflpesfdgdpasnt---aplqpeqlqvfetleeitgylyisawpd
                                                                                                                                      LRMQPG--PAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPI-----SPVSVGRGPD
                                                                                                                                                                                YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCAR----GTHSLLPRPAAVPVP
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83.0%;
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Pred. No. 4e-143;
9; Mismatches 45;
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self-protein;
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; cancer; breast cancer; prostate cancer;
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/note= "suitable for for
695..709
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653..667
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624..654
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5..25
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suitable for for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     helper epitopes were identified (see features table). The method is used for inducing immune responses against weakly immunogenic cell-associated peptide antigens (PA) such as those associated with cancers (self-proteins), e.g. human prostate specific membrane antigen (PSM), heregulin 2 (Her2) and/or fibroblast growth factor 8b (PGF8b). The method comprises effecting simultaneous presentation by antigen producing cells (APCs) of the animals immune system of: (1) at least 1 CTL (cytotoxic T-lymphocyte) group derived from the PA and/or at least 1 first T helper cell group which is foreign to the animal. Analogues of human PSM, human Her2 and human/murine FGF8b comprising a substantial part of all known and predicted CTL and B-cell epitopes of the respective PA and including at least or part of all known and predicted CTL and B-cell epitopes are also claimed. The method is used to treat prostate, prostate/breast or breast cancer when the PA is human PSM, FGF8b and Her2, respectively.
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          response. Subdominant CTL epitopes, antibody binding regions and cysteine residues involved in disulfide bonds are preserved in the immunogenized forms. Regions suitable for the insertion of foreign T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 62; Page 193-198; 220pp; English.
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20-0CT-1998;
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eltylptnas1sf1qdiqevqgyvliahnqvrqvplqrlrivrgtqlfednyalavldng
                                                                                                                                                                                                                                                                                               can be used in the claimed method as an autovaccine to induce a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is the human heregulin 2 (Her2) sequence. Immunogenic analogues
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                                                           aagctgpkhsdclaclhfnhsgicelhcpalvtyntdtfesmpnpegrytfgascvtacp
                                                                                                                                   LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
                                                                                                                                                                                                                                                      ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
                                                                          AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
                                                                                                                    ltlidtnrsrachpcspmckgsrcwgessedcqsltrtvcaggcarckgplptdccheqc
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98US-0105011
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Pred. No. 4e-143;
9; Mismatches 4
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                                                                                                                                                     Matches 362;
                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                            The invention provides an isolated antigen-presenting cell, which expresses at least an immunogenic portion of a polypeptide that produces an immune response to HER-2/neu protein. The antigen-presenting cells are useful as vaccines for eliciting or enhancing an immune response to HER-2/neu protein, particularly in treating or preventing malignancies in which the HER-2/neu oncogene is associated. Specifically, these are useful for treating or preventing cancer, e.g. breast cancer, ovarian, colon, lung or prostate cancers. The present sequence represents the human HER-2/neu protein (also known as p185 or c-erbB2).
                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cheever MA,
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                                                                                                                                                                                                                                                                                                                                                                                                          New antigen-presenting cells, useful as vaccines for eliciting or enhancing an immune response to HER-2/neu protein, particularly useful for treating or preventing cancer, e.g. breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200153463-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antigen-presenting cell; immunogenic; i oncogene; cancer; cytostatic; vaccine;
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                                                     ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
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DB; AAH23392.
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Pred. No. 4e-1
9; Mismatches
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; p185; c-erbB2.
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RESULT 15
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XX AAG882
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AKW HUMBAN;
KW HUMBAN;
KW IMMUNE
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The present invention describes isolated prepared HER2/neu epitopes (I).

Calso described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is culture in vitro and binds to a complex of an epitope (I), bound to a complex of an epitope (I) bound to a complex of an epitope (I) bound to a complex of a contiguous amino cards that have 100% identity with a native peptide sequence of HER2/neu; (3) a vaccine composition (III) comprising (I) and a pharmaceutical cardinent; (4) an isolated nucleic acid encoding a peptide comprising (I); and (5) an isolated nucleic acid encoding (II). (I) has cytostatic and immunostimulant activities, and can be used in vaccines. (I), (II) cand (III) are useful for inducing cellular immune responses for the prevention and treatment of cancer. (I) and (II) are useful for monitoring or evaluating an immune response to a tumour-associated cantigen when incubated with a T lymphocyte sample form a patient and
                                                                                                                                                                                                                                                                                                                                                                                                                                                             An isolated prepared HER2/neu cellular immune responses for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; HER2/neu; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure;
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id antigen; T lymphocyte; cytotoxic T lymphocyte;
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Matches 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                detecting the presence of bound T lymphocyte to (I) or (II). Epitope based vaccines mean that immunosuppressive epitopes that may be present in whole antigens may be avoided. Selected epitopes may be combined to enhance immunogenicity. The possible pathological side effects caused by infectious agents or whole protein antigen is eliminated. The vaccine provides the ability to direct and focus an immune response to multiple selected antigens from the same pathogen. Epitope-based anti-tumour vaccines provides the opportunity to combine epitopes derived from multiple tumour-associated molecules addressing the problem of tumour tumour variability and reducing the likelihood of tumour escape due to antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in the exemplification of the present invention.
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                                                                          LRMQPG--PAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPI-----
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GenCore version 4.5 Copyright (c) 1993 - 2000 Com Compugen

OM protein - protein search, using sw model

April 11, 2002, 09:30:07; Search time 25.01 Seconds

(without alignments)
1276.175 Million cell updates/sec

Title: Perfect score: US-09-234-208B-2 2287

MELAALCRWGLLLALLPPGA.....VGRGPDPDAHVAVNLSRYEG

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 segs, 76174552 residues

Total number of hits satisfying chosen parameters:

Minimum DB Maximum DB seq length: 0

length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database PIR_68:* pir1:*
pir2:*
pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	0	ر ت	4	ω	2	_	NO.	Result
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5.7	1 . 2 . 3 .	5.8	6.0	6.2	6.3	7.0	8.9	9.9	10.3	10.9	11.0	11.3	11.3	11.4
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subtilisin-like pr	MEGF6 protein - ra	subtilisin-like pr	hypothetical prote	agrin - rat	serine proteinase	furin (EC 3.4.21.7	insulin receptor h	tyrosine kinase re	insulin-like growt	insulin receptor-r	insulin-like growt	insulin-like growt	insulin receptor -	insulin receptor p

ALIGNMENTS

C;Species: Homo sapiens (man)
C;Date: 25-Oct-1987 #sequence_revision 06-Dec-1996 #text_change 11-Jun-1999
C;Accession: A24571; A25491; A44188; B44188; I59509; I57622 N;Alternate names: c-erb-B-2 protein precursor; kinase-related transforming protein e protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - human

R;Yamamoto, T.; Ikawa, S.; Akiyama, T.; Semba, K.; Nomura, N.; Miyajima, N.; Saito, Nature 319, 230-234, 1986

A; Title: Similarity of protein encoded by the human c-erb-B-2 gene to epidermal growt A; Reference number: A24571; MUID:86118663

A; Accession: A24571

A; Molecule type: mRNA A; Residues: 1-1255 < YAM>

A;Cross-references: GB:X03363; NID:g31197; PIDN:CAA27060.1; PID:g31198 R;Semba, K.; Kamata, N.; Toyoshima, K.; Yamamoto, T. Proc. Natl. Acad. Sci. U.S.A. 82, 6497-6501, 1985 A;Title: A v-erbB-related protooncogene, c-erbB-2, is distinct from the c-erbB-1/epid A;Reference number: A25491; MUID:86016729 A;Accession: A25491

A; Molecule type: DNA A; Residues: 737-1031 SEM>

R; Coussens, L.; Yang-Feng, T. Science 230, 1132-1139, 1985 A;Cross-references: GB:M11767; NID:g182163; PIDN:AAA35808.1; R;Coussens, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, E.; Gray, PID:g553282 A.; McGrath, McGrath, J.; Seeburg

A;Title: Tyrosine kinase receptor with extensive homology to EGF receptor shares chro A;Reference number: A44188; MUID:86070181
A;Accession: A44188

A; Molecule type: DNA A; Residues: 740-910 <COUI>

A;Cross-references: GB:M12036; NID:g183988; PIDN:AAA35978.1; PID:g183989 A;Accession: B44188

A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-517, 'RALL',522,'S',524-654,'V',656-1169,'A',1171-1255 <COU2>
A;Residues: 1-517, 'RALL',522,'S',524-654,'V',656-1169,'A',1171-1255 <COU2>
A;Cooss-references: GB:M11730; NID:g183986
R;King, C.R.; Kraus, M.H.; Aaronson, S.A.
Science 229, 974-976, 1985
Science 229, 974-976, 1985
A;Title: Amplification of a novel v-erbB-related gene in a human mammary c:
A;Reference number: 159509; MUID:85272597
A;Accession: 159509

a human mammary carcinoma.

A;Status: translated from GB/EMBL/DDBJ

Givol,

A;Molecule type: DNA
A;Residues: 83-909 <REX>
A;Residues: 83-909 <REX>
A;Cross-references: GB:L29395; NID:g459807; PIDN:AAA35809.1; PID:g459808
A;Cross-references: GB:L29395; NID:g459807; PIDN:AAA35809.1; PID:g459808
A;Cross-references: GB:L29395; NID:g459807; PIDN:AAA35809.1; PID:g459808
M; King, C.R.; Kraus, M.H.; Ullrich, A.; Schlessinger, J.; Givol.
Mol. Cell: Biol. 7, 2597-2601, 1987
A;Title: Human HERZ (neu) promoter: evidence for multiple mechanisms for A;Reference number: 157622; MUID:87286898 for multiple mechanisms for transcriptio

A;Status: translated from GB/EMBL/DDBJA;Molecule type: DNA A; Accession: I57622

type: DNA : 1-191 <TAL>

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A;Cross-references: GB:M16792; NID:g183983; PIDN:AAA58637.1; PID:g553332
C;Comment: Amplification and overexpression of this erbb-related gene occurs in about 3C;Comment: Amplification and overexpression of this erbb-related gene occurs in about 3C;Comment: Amplification and overexpression of this erbb-related gene occurs in about 3C;Comment: Amplification: 17q21.1-17q21.1
A;Cross-references: GDB:120613; OMIM:164870.
A;Map position: 17q21.1-17q21.1
A;Introns: 25/1; 75/3; 147/1; 883/3
A;Note: the list of introns is incomplete
C;Function:
A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C;Councilon: catalyzes the phosphorylation; protein kinase homology
C;Keywords: ATP; autophosphorylation; duplication; protein; phosphorotein; phosphoroteinse
F;22-1255/Product: protein-tyrosine kinase predicted <STC>
F;22-1255/Product: protein-tyrosine kinase erbb2 *status predicted <MAT>
F;21-653/Domain: Eggr receptor extracellular domain repeat <EEE>
F;395-605/Domain: Eggr receptor extracellular domain repeat <EEE>
F;395-605/Domain: brotein kinase homology <KINSP
F;764-755/Domain: protein kinase homology <KINSP
F;765-734/Region: protein kinase ATP-binding motif
F;68,114,187,259,530,571,629/Binding site: carbohydrate (Asn) (covalent) *status predicted F;753/Active site: Lys *status predicted (Tyr) (covalent) (by autophosphorylation)
F;1139,1221,1222,1248/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation)
protein-tyrosine kinase (EC 2.7.1:112) new precursor C; Species: Rattus norvegicus (Norway rat) C; Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #t C; Accession: A24562; A61204 R; Bargmann, C.I.; Hung, M.C.; Weinberg, R.A. Nature 319, 226-230, 1986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLPDLSVFQNLQVIRG
                                                                                                                                                                                                                                                 -- PDAHVAVNLSRYEG
                                                                                                                                                                                                                                                                                                                               LRMQPG--PAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPI-----
                                                                                                                                                                                                                                                                                                                                                                       YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN
                                                                                                                                                                                                                                                                                                                                                                                            YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCAR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGCTGPKHSDCLACLHENHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
                                                                                                                                                                                                                                                                                   IQEFAGCKKIFGSLAFLPESFDGDPASNT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              362;
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83.0%;
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Pred.
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No. 4
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                                                          #text_change
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                                                            11-Jun-1999
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p-185 precursor - golden hamster C;Species: Mesocricetus auratus (golden hamster) C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 C;Accession: I48161

A; Accession: I48161 A; Status: prelimina A; Molecule type: mR

preliminary;

translated

from

GB/EMBL/DDBJ

Gene 140, R; Nakamura, T.;

251-255,

Ushijima,

T.;

Ishizaka,

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Nagao,

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Ishika

#text_change 18-Jun-1999

A; Title: Cloning and A; Reference number: 1

I48161; activation

MUID: 94193007

of.

the

hamster

neu Arai,

proto-oncogene

RESULT 148161

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A;Gene: neu
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phospho;
F;1-19/Domain: signal sequence #status predicted <SIG>
F;10-1260/Product: protein-tyrosine kinase neu #status predicted <MAT>
F;20-1260/Product: protein-tyrosine kinase neu #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: A61204; MUID:92035293
A;Status: Note: No
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A; Residues: 1-1260 «BAR>
A; Cross-references: EMBL:X03362; NID:g56745; PIDN:CAA27059.1; PID:g56746
A; Cross-references: EMBL:X03362; NID:g56745; PIDN:CAA27059.1; PID:g56746
R; Masul, T.; Mann, A.M.; Macatee, T.L.; Garland, E.M.; Okamura, T.; Smitl
Carcinogenesis 12, 1975-1978, 1991
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F;723-988/Domain: protein kinase homology <KINN
F;731-739/Region: protein kinase homology <KINN
F;731-739/Region: protein kinase ATP-binding motif
F;71,191,263,535,576,634/Binding site: carbohydrate (Asn) (covalent)
F;691/Binding site: phosphate (Thr) (covalent) #status predicted
F;758/Active site: Lys #status predicted
F;758/Active site: Lys #status predicted
F;758/Active site: Lys #status predicted
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C; Genetics:
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A; Residues: 637-663,'V',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MELAALCRWGILLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
                                 PYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARGTHSL
                                                                                                                                                                                          CAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTAC
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PYNYLSTEVGSCTLVCPPNNQEVTAEDGTQRCEKCSKPCARVCYGL
                                                                                                                                                     CAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMHNPEGRYTFGASCVTTC
                                                                                                                                                                                                                                                                                                                  APVDIDTNRSRACPPCAPACKDNHCWGESPEDCQILTGTICTSGCARCKGRLPTDCCHEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELTYVPANASLSFLQDIQEVQGYMLIAHNQVKRVPLQRLRIVRGTQLFEDKYALAVLDNR 123
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Pred. No. 1.3
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A;Accessrum. A;Accessrum. A;Molecule type: mRNA
A;Residues: 1-123 <LAX>
A;Cross-references: GB:M20386
A;Cross-references: GB:M20386
R;NISen, T.W.; Maroney, P.A.; Goodwin, R.(Cell 41, 719-726, 1985
A;Title: c-erbB activation in ALV-induced (Cell 41, 719-76479000)
A;Title: A;Carence number: A00643; MUID:85228222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               epidermal growth factor receptor precursor - chicken
N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB
C;Species: Gallus gallus (chicken)
C;Date: 28-Feb-1986 #sequence_revision 05-May-1995 #text_change 04-Feb-2000
C;Accession: A27720; A00643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-1254 <RES>
A; Cross-references: GB:D16295; NID:g493236; PIDN: A; Cross-references: GB:D16295; NID:g493236; PIDN: C; Genetics: A; Gene: neu C; Superfamily: epidermal growth factor receptor; C; Keywords: ATP E; 718-983/Domain: protein kinase homology <KIN> F; 726-734/Region: protein kinase ATP-binding motifications of the complex of the
                                                                                       C; Superfamily: epidermal growth fact; Keywords: alternative splicing;
                                                                                                                         A; Gene: erbB
C; Superfamily
                                                                                                                                                                                                                                            A; Reference number: A00643;
A; Accession: A00643
A; Molecule type: mRNA
A; Residues: 585-1223 <NIL>
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                                                              pecific protein kinase
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A; Accession: A27720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Chicken epidermal growth factor (EGF) receptor: cDNA cloning, expression A;Reference number: A27720; MUID:88261272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Lax, I; Johnson, A; Howk, R; S
Mol. Cell. Biol. 8, 1970-1978, 1988
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;1-30/Domain: signal sequenc
;31-1223/Product: epidermal
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                                                                                       epidermal growth factor ternative splicing; ATP;
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                                  sequence #status
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kinase ATP-binding motif
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Pred. No. 4.6e-100;
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factor receptor #status
                                                                                       receptor; protein kinase homology
autophosphorylation; glycoprotein;
                                  predicted
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LLLLLLGRVALCSAVEEKKVCQGTNNKLTQLGHVEDHFTSLQRMYNNCEVVLSNLEITYV 79

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Mol. Cell. Biol. 12, 883-893, 1992
A;Title: An alternatively processed mRNA from A;Reference number: A42032; MUID:92123214
A;Accession: A42032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
A42032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;719-984/Domain: protein kinase homology <KIN>
F;727-735/Region: protein kinase ATP-binding motif
F;727-735/Region: protein kinase ATP-binding motif
F;136,202,280,361,370,422,575,580,615,635/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;192,550/Binding site: carbohydrate (Ser) (covalent) (by protein kinase C) #status predicte
F;687/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #s
F;1100,1183,1208/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #s
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F:81-307/Domain: EGF receptor extracellular domain repeat
F:397-610/Domain: EGF receptor extracellular domain repeat
F:397-655-677/Domain: transmembrane #status predicted <TMM>
F:678-1223/Domain: intracellular #status predicted <INT>
Qy
                                                                                                                                                A;Experimental source: liver
A;Note: sequence extracted from NCBI backbone (NCBIN:76892, NCBIP:76893)
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATP; growth factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                         epidermal growth factor receptor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Jun-1999
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A; Residues: 1-527 <FLI>
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                                                                                                                                                                                                                                                                                               A; Status: preliminary
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Pred. No. 5.6e
55; Mismatches
                                             Score 794; DB 2;
Pred. No. 3.4e-47;
5; Mismatches 109
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A;Title: Human epidermal growth factor receptor cDNA sequence and aberrant ex A;Title: Human epidermal growth factor receptor cDNA sequence and aberrant ex A;Reference number: A00641; MUID:84219729
A;Recession: A00641
A;Relecule type: mRRA
A;Residues: 1-1210 <ULL>
A;Rolecule type: mRRA
A;Residues: 1-1210 <ULL>
A;Rolecule type: mRRA
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                                                                                                                                                                                                                               A; Title: Human epidermal growth factor receptor A; Reference number: A00642; MUID:84245835 A; Accession: A00642
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;Molecule type: mRNA;Molecule type: mRNA; Molecule type: mRNA;Residues: 'RCAWRRA',150-187,'KSVIQAV',195,'M',197,'A',199-222,'S',224-304,'RA';Residues: 'RCAWRRA',150-187,'KSVIQAV',195,'M',197,'A',199-222,'S',224-304,'RA'; Typerimental source: A431 human carcinoma cells, which have large numbers of Elemental source: A431 human carcinoma cells, which have large numbers of Elemental source: A431 human carcinoma cells, which have large numbers of Elemental source: A431 human carcinoma cells, which have large numbers of Elemental source: A431 human carcinoma cells, which have large numbers of Elemental source: A431 human carcinoma cells, which have large numbers of Elemental source: A431 human carcinoma cells, which have large numbers of Elemental source: A431 human carcinoma cells, which have large numbers of Elemental source: A431 human carcinoma cells, which have large numbers of Elemental source: A431 human carcinoma cells, which have large numbers of Elemental source: A431 human carcinoma cells, which have large numbers of Elemental source: A431 human carcinoma cells, which have large numbers of Elemental source: A431 human carcinoma cells, which have large numbers of Elemental source: A431 human carcinoma cells, which have large numbers of Elemental source: A431 human carcinoma cells, which have large numbers of Elemental source: A431 human carcinoma cells, which have large numbers of Elemental source: A431 human carcinoma cells, which have large numbers of Elemental source: A431 human carcinoma cells, which have large numbers of Elemental source: A431 human carcinoma cells, which have large numbers of Elemental source: A431 human carcinoma cells, which have large numbers of Elemental source: A431 human carcinoma cells, which have large numbers of Elemental source: A431 human carcinoma cells, which have large numbers of Elemental source: A431 human carcinoma cells, which have large numbers of Elemental source numbers of Elemental source numbers of Elemental source numbers of Elemental source numbers of Elementa
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C; Genetics:
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A; Experimental source:
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R;Mroczkowski, B.; Mosig, G.; Conen, S.

Nature 309, 270-273, 1984
A;Title: ATP-stimulated interaction between epidermal
A;Reference number: A38023; MUID:84191554
A;Contents: annotation; receptor activity
A;Note: the EGF receptor (and other tyrosine kinases)
A;Note: the EGF receptor (and other tyrosine kinases)
R;Chen, W.S.; Lazar, C.S.; Lund, K.A.; Welsh, J.B.; Ch
Cell 59, 33-43, 1989
                                                                                                                                                                                                                                                 A.Map position: 7p12.3-7p12.1
C.Superfamily: epidermal growth factor receptor; protein kinase homology C.Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphor F.1-24/Domain: signal sequence #status predicted <SIG>F; 25-1210/Product: EGF receptor #status predicted <MAT>F; 25-645/Domain: extracellular #status predicted <EXT>F; 75-300/Domain: EGF receptor extracellular domain repeat <EE1>F; 390-600/Domain: EGF receptor extracellular domain repeat <EE2>F; 646-668/Domain: transmembrane #status predicted <TMM>F; 646-668/Domain: intracellular #status predicted <INT>
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A;Accession: A60143
A;Molecule type: protein
A;Residues: 740-744,'X',746-747 <RUS>
A;Residues: 740-744,'X',766-747 <RUS>
                                                                                                                 F;1047-1210/Region: inhibitory F;128,175,352,413,444,528,603/Binding site: F;745/Active site: Lys \#status experimental
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A; Title: Expression cloning
A; Reference number: A43615;
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A;Cross-references: GDB:120610;
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A; Residues: 25-30, 'S', 32-51; 454-467
R; Russo, M.W.; Lukas, T.J.; Cohen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: A05281; MUID:84172183 A;Accession: A05281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1028-1210 <SIM
R; Weber, W.; Gill, G.N.; S
Science 224, 294-297, 1984
                                                                                                                                                                                     F;999-1046/Region: coated-pit mediated internalization signal
                                                                                                                                                                                                        F;710-975/Domain: protein kinase homology <KIN>F;718-726/Region: protein kinase ATP-binding mo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: Functional independence of the epidermal A; Reference number: A33331; MUID:90003233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ental source: epidermoid carcinoma cell F.A.; Gope, M.L.; Schulz, T.Z.; Wright, Biophys. Res. Commun. 124, 125-132, 1984
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er: A23062;
Conservative
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    50;
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  Score 793; DB
Pred. No. 9.7e-
50; Mismatches
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right, D.A.; Carpenter,
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, C.P.; Walton, G.M.;
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A;Molecule type: protein
A;Molecule type: protein
A;Residues: 689-694,'X',696-704,'L',706-707;989-992,'XX',995-996,'X',998-1000;1002-1009
A;Residues: 689-694,'X',696-704,'L',706-707;989-992,'XX',995-996,'X',998-1000;1002-1009
A;Hibbs, M.L.; Dunn, A.R.; Alexander, W.S.
Submitted to the EMBL Data Library, April 1994
A;Description: The complete cDNA sequence of the Mouse Epidermal Growth Factor Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 969-971, 'K', 973-1115,'D' <EIS>
A; Cross references: EMBL: Z12608
R; Heisermann, G.J.; Gill, G.N.
J. Biol. Chem. 263, 13152-13158, 1988
A; Title: Epidermal growth factor receptor threonine and A; Reference number: A28941; MUID: 88330814
A; Accession: A28941
A;Gene: EGFR
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATP; growth factor receptor; kinase-related transforming pro
                                                                                                                                                                                   A;Cross-references: EMBL:X78987; NID:g488830; PIDN:CAA55587.1; PID:g488831 R;Paria, B.C.; Das, S.K.; Andrews, G.K.; Dey, S.K. Proc. Natl. Acad. Sci. U.S.A. 90, 55-59, 1993 A;Title: Expression of the epidermal growth factor receptor gene is regula A;Reference number: 149643; MUID:93126380
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                                                                         A;Cross-references: GB:L06864; C;Genetics:
                                                                                                                A;Status: translated from GB/E
A;Molecule type: mRNA
A;Residues: 12-20,22-132 <RES>
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A; Residues: 1-971, 'K', 973-1210 <VER>
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A; Residues: 1-714 < AVI>
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A;Accession: A43818
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Oncogene 6, 673-676, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-1210 <LUE>
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                                                                                              NID: g193001; PIDN: AAA53029.1;
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      protein;
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A; Residues: 1-644 < PET>
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Best Local Similarity
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  PLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLAL
                                                                                                                                                            LAALCAAG-----GALEEKKVCQGTSNRLTQLGTFEDHFLSLQRMFNNCEVVLGNLE
                                                                                                                                                                                                   LAALCRWGLLLALLPPGA-ASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLE 61
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                                                                                                                LTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGD 121
                                                                       ITYVQRNYDLSFLKTIQEVAGYVLIALNTVERIPLENLQIIRGNALYENTYALAVLSN--
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44;

23;

Gaps

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124

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F:1-24/Domain: signal sequence #status predicted <SIG>
F;648-670/Domain: transmembrane #status predicted <TMM>
F;648-670/Domain: protein kinase homology <KIN>
F:712-977/Domain: protein kinase homology <KIN>
F:720-728/Region: protein kinase ATP-binding motif
F:680,695/Binding site: phosphate (Thr) (covalent) #status experimental
F:697,1070,1071/Binding site: phosphate (Ser) (covalent) #status experimental
F:993/Binding site: (or 997) phosphate (Ser) (covalent) #status experimental
F:1028/Binding site: (or 1030 or 1032) phosphate (Ser) (covalent) #status experimental
F:1197/Binding site: phosphate (Tyr) (covalent) #status experimental
                                                                                                            C; Superfamily: epidermal growth factor receptor; protein kinase C; Keywords: alternative splicing; ATP; growth factor receptor \Gamma
                                                                                                                                                                                                                                                                                                                                                                                                                         epidermal growth factor receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Jan-1991 #sequence_revision 25-Jan-1991 #text_change 10-Oct-1997
C;Accession: A36325
                                                                                                                                                                                                                                                                                                                A; Reference number: A36325; MUID: 90258888
                                                                                                                                                                                                                                                                                                                                          Cell. Biol. 10, 2973-2982, 1990 the: A truncated, secreted form of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDI----FHKNNQLALTLI 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGPRESDCLVCQKFQDEATCKDTCPPLMLYNPTTYQMDVNPEGKYSFGATCVKKCPRNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VVTDHGSCVRACGPDYYEV-EEDGIRKCKKCDGPCRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -YGTNRTGLRELPMRNLQEILIGAVRFSNNPILCNMDTIQWRDIVQNVFMSNMSMDL---
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                                                                                                                                                                         GB:M37394
  34.2%;
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Score 781.5; DB 2;
Pred. No. 3.1e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 789; DB 2; Pred. No. 1.8e-46;
                                                                                                                                                                                                                                                                                                                                                                                               V.W.; Blasband, A.;
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                             Length
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epidermal growth factor receptor, HER4 - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;pate: 22-Sep-193 #sequence_revision 18-Nov-1994 #text_C;Accession: A47253 R;Plowman, G.D.; Culouscou, J.M.; Whitney, G.S.; Green, J Proc. Natl. Acad. Sci. U.S.A. 90, 1746-1750, 1993 A;Title: Ligandr-specific activation of HER4/p180erbB4, a A;Reference number: A47253; MUID:93189574 A;Accession: A47253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: nucleic acid
A; Residues: 1-1308 cptD>
A; Residues: 1-1308 cptD>
A; Residues: 1-1308 cptD>
A; Note: sequence extracted from NCBI backbone (NCBIP:126842)
A; Note: sequence extracted from NCBI backbone (NCBIP:126842)
C; Superfamily: epidermal growth factor receptor; protein kinase homology
C; Keywords: ATP; growth factor receptor
F; 716-981/Domain: protein kinase homology <KIN>
F; 724-732/Region: protein kinase ATP-binding motif
                 C:Species: Homo sapiens (man)
C:Date: 04-Oct-1991 #sequence_revision
C:Accession: A36223; I59164
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Best Local Similarity
Matches 157; Conser
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   M.H.;
                                                                                                                                                                      V-VDSSSCVRACPSSKMEV-EENGIKMCKPCTDICPKACDGIGTGSLM
                                                                                                                                                                                                         LSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCAR----GTHSLL
                                                                                                                                                                                                                                         DTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHEQCAAG
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                                                                                                                                                                                                                                                                                  CTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNY
                                                                                                                                                                                                                                                                                                                     STNGSSGCGRCHKSCTG-RCWGPTENHCQTLTRTVCAEQCDGRCYGPYVSDCCHRECAGG
                                                                                                                                                                                                                                                                                                                                                                                                                  NTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IEHNRDLSFLRSVREVTGYVLVALNQFRYLPLENLRIIRGTKLYEDRYALAIFLNYRKDG
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   Issing,
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                                                                                                                                                                                                                                                                                                                                                                                              -GLQELGLKNLTEILNGGVYVDQNKFLCYADTIHWQDIVRNPWPSNLTLV
W.; Miki,
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45.1%;
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 T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 775; DB 2;
Pred. No. 1.8e-45;
                                                                           (erbB3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
Popescu,
                                        13-Jan-1993
                                                                         (EC 2.7.1.-)
 N.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124;
                                      #text_change 17-Nov-2000
   Aaronson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1308;
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                                                                         precursor -
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   S.A.
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epidermal growth factor receptor homolog precursor - rat
N;Alternate names: ErbB3 protein; HER3 protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 13-Nov-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 12q13-12q13
C;Superfamily: unassigned Ser/Thr or Tyr-specific C;Keywords: ATP; phosphotransferase E;707-972/Domain: protein kinase homology <KIN>E;715-723/Region: protein kinase ATP-binding motif
A; Molecule type: mRNA
A; Residues: 1-1339 < HEL>
A; Cross-references: GB:U29339;
A; Experimental source: liver
A; Note: The authors translated
                                                                                                A; Title: Cloning of the rat A; Reference number: JC4387; A; Accession: JC4387
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A;Molecule type: mRNA
A;Residues: 1-559, 'G',561-957,'F',959-1063,'G',1065-1342 <RES
A;Cross-references: GB:M34309; NID:g183990; PIDN:AAA35979.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 86, 9193-9197, 1989 A;Title: Isolation and characterization of ERBB3, A;Reference number: A36223; MUID:90083234 A;Accession: A36223
                                                                                                                                                        Gene 165, 279-284, 1995
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A; Cross-references: GB:M29366
                                                                                                                                                                           R; Hellyer, N.J.; Kim,
                                                                                                                                                                                                 C; Accession: JC4387
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Best Local S
Matches 150
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                                                                                                                                                                                                                                                                                                                                                                                DQTSCVRACPPDKMEVD-KNGLKMCEPCGGLCPKACEGTGS
                                                                                                                                                                                                                                                                                                                                                                                                                       DVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCAR---GTHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTN 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLLLALLPPGAA---STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PQDTDCFACRHFNDSGACVPRCPQPLVYNKLTFQLEPNPHTKYQYGGVCVASCPHNFV-V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHEQCAAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----NSSHALRQLRLTQLTEILSGGVYIEKNDKLCHMDTIDWRDIVRDRD----AEIVVKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NADLSFLQWIREVTGYVLVAMNEFSTLPLPNLRVVRGTQVYDGKFAIFVM-----LNYNT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150;
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                                                                                                                                                                             н.н.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32.2%;
                                                                                                                       ErbB3 cDNA and MUID:96096535
                                                                                                                                                                               Greaves, C.H.;
                                     NID:g915389; PID:g915390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 735.5; DB 2;
Pred. No. 9.5e-43;
9; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of ERBB3, a third member of
                                                                                                                                          characterization
                                                                                                                                                                               Sierke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           motif
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                                                                                                                                                                               S.L.;
                                                                                                                                                                                                                                                                                                                                                                                  336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             epidermal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                          the
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C;Comment: This protein is a numerical C;Genetics:
C;Genetics:
A;Gene: ErbB3
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; |
C;Keywords: ATP; growth factor receptor: liver; phosphoprotein; tra.
F;1-19/Domain: signal sequence #status predicted <SIG-
F;20-1339/Product: epidermal growth factor homolog #status predicte
F;640-659/Domain: transmembrane #status predicted <TMM>
F;713-721/Region: protein kinase ATP-binding motif
F;939,1051,1156,1194,1196,1219,1257,1259,1273,1286,1325/Binding sit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Nolecule type: DNA
A; Molecule type: DNA
A; Mesidues: 1-1166 <WIT>
A; Residues: 1-1166 <WIT>
A; Cross-references: EMBL: X16891; NID: 965290; PIDN: CAA34770.1;
A; Cross-references: EMBL: X16891; PIDN: CAA34770.1;
A; Cross-references: EMBL: X16891; PIDN: CAA34770.1;
A; Cross-references: EMBL: X16891; PIDN: CAA34770.1;
A; Cross-
A;Gene: mrk
A;Map position: Y
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A;Map position: Y
A;Introns: 872/3; 898/1; 947/1; 979/3; 1025/3; 1056/1
A;Introns: 872/3; 898/1; 947/1; 979/3; 1025/3; 1056/1
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATP; growth factor receptor; phosphotransferase; transmembrar
F;1-25/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                 R; Adam, D.; Maeueler, W.; Schartl, M.
Oncogene 6, 73-80, 1991
A; Title: Transcriptional activation of the melanoma inducing X
A; Reference number: $13807; MUID:91125882
A; Accession: $13809
A; Status: preliminary; translation not shown
A; Molecule type: DNA
A; Residues: 821-1025, 'N', 1027-1098, 'A', 1100-1166 <ADA>
A; Cross-references: EMBL:X56319; NID:965284; PIDN:CAA39763.1;
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein-tyrosine kinase (EC 2.7.1.112) mrk-Y precursor - southern platyfish X;Alternate names: epidermal growth factor receptor homolog; kinase-related C;Species: Xiphophorus maculatus (southern platyfish) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 18-Feb-2000 C;Accession: S06142; S13809 R;Wittbrodt, J; Adam, D.; Malitschek, B.; Maeueler, W.; Raulf, F.; Telling, Nature 341, 415-421, 1989 R;Wittbrodt, J; Adam, D.; Malitschek, Bh; Maeueler, W.; Raulf, F.; Telling, N;Title: Novel putative receptor tyrosine kinase encoded by the melanoma-ind A;Reference number: S06142; MUID:90015140 A;Accession: S06142
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Pred. No. 9.1e-40;
6; Mismatches 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query
Best I
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300
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CPSNYVVTE-GACVRSCSAGMLEVD-ENGKRSCKPCDGVCPK
                   CPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCAR
                                                                      HCAGGCTGPRATDCLACRDFNDDGTCKDTCPPPKIYDIVSHQVVDNPNIKYTFGAACVKE
                                                                                         QCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTA
                                                                                                                                             TMNLIPHAFERQCQKCDHGCVNGSCWAPGPGHCQKFTKLLCAEQCNRRCRGPKPIDCCNE
                                                                                                                                                                                                                                          GDPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQL
                                                                                                                                                                                                                                                                                            LEITYTQENQDLSFLQSIQEVGGYVLIAMNEVSTIPLVNLRLIRGQNLYEGNFTLLVMSN
                                                                                                                                                                                                                                                                                                             LELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDN 119
                                                                                                                                                                                                                                                                                                                                                                                                     AALCRWGLLLALLPPGAAST----QVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGN
                                                                                                                                                                                                                    YQK-NPSSP--DVYQVGLKQLQLSNLTEILSGGVKVSHNPLLCNVETINWWDIVDKTSNP
                                                                                                                                                                                                                                                                                                                                                                     AALLQ - - LLLVLSISRCCSTDPDRKVCQGTSNQMTM - - - LDNHYLKMKKMYSGCNVVLEN
                                                                                                                                                                             ALTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGC-ARCKGPLPTDCCHE
                                                                                                                                                                                                                                                                                                                                                                                                                                          al Similarity
145; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 681.5; DB 1
Pred. No. 4.1e-39;
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339
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                                                                                                                                                                                                                                                                                                                                                                     62
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A; Gene: FlyBase:Egfr A; Cross-references: Fl C; Superfamily: epiderr C; Keywords: ATP; growt A; Fittle: Alternative 5' exon A; Reference number: A27131; A; Accession: A27131 A; Moleculo: *** C; Accession: A27131 R; Schejter, E.D.; S epidermal growth factor receptor - fruit fly (Drosophila melanog C;Species: Drosophila melanogaster C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change C; Genetics: A; Molecule type: mRNA A; Residues: 1-843 <SC Cross-references: FlyBase:FBgn0003731; Superfamily: epidermal growth factor Matches Query Match Best Local 215 198 155 138 111 83 51 24 SCTHG-CWGEGPKNCQKFSKLTCSPQCAGGRCYGPKPRECCHLFCAGGCTGPTQKDCIAC YVLIAHNQVRQVPLQRLRIVRGTQLF----EDNYALAVLDNGDPLNNTTPVTGASPGGL 137 QVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPT-NASLSFLQDIQEVQG MCKGSRCWGESSEDCQSLTRTVCAGGCA--RCKGPLPTDCCHEQCAAGCTGPKHSDCLAC YTLEIPDLRDVLNGQVGFHNNYNLCHMRTIQWSEIVSNGTDAYYNYDFTAPERECPKCHE RELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSP YILISHVDVKKVVFPKLQIIRGRTLFSLSVEEEKYALFV-119; Similarity epidermal growth factor
P; growth factor receptor Conservative Segal, <SCH> exons and tissue-specific expression 131; MUID:87002474 D.; Glazer, 25.2%; 45; Score 575.5; pred. No. 5.4e 45; Mismatches fruit fly (Drosophila melanogaster) (fragment) ٢ receptor; Shilo, υB 2; 5.4e-32; es B protein Indels Length kinase of. 31; the Drosophila 23-May-1997 homology -TYSKM Gaps 255 197 154 110 273 214 82 7; EGF re

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A;Map position: 2

A;Map position: 2

A;Map position: 2

A;Map position: 2

A;Athrons: 44/1; 51/1; 90/1; 112/3; 165/3; 217/1; 290/1; 379/1; 418/1; 448/2; 565/1; 60

C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homol

C;Reywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein by: 1-28/Domain: signal sequence #status predicted <SIG>
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-1374/Product: protein tyrosine kinase let-23 #status predicted <MAT>
F;934-1199/Domain: protein kinase homology <KIN>
F;942-950/Region: protein kinase ATP-binding mottif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein-tyrosine kinase (EC 2.7.1.112) let-23 precursor N;Alternate names: receptor tyrosine kinase let-23 C;Species: Caenorhabditis elegans C;Date: 21-Apr-1997 #sequence_revision 09-May-1997 #text C;Accession: $70712; $73101; $13422; T27682
                                                                Дb
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A;Residues: 52-1374 <WIL>
A;Residues: 52-1374 <WIL>
A;Cross-references: EMBL:Z70038; PIDN:CAA93882.1; GSPDB:GN00020; CESP:ZK1067.1
A;Experimental source: clone ZK1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data A; Reference number: 220404 A; Accession: T27682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 52-1374 < ARO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: The let-23 gene necessary for Caenorhabditis elegans vulval A;Reference number: $13422; MUID:91080919
A;Accession: $13422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:D63426; NID:g1407562; PIDN:BAA09729.1; PID:d1010375; PID:g1407 A;Experimental source: strain N2 R;Arolan, R.V.; Koga, M.; Mendel, J.E.; Ohshima, Y.; Sternberg, P.W. Nature 348, 693-699, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: S73101
A;Molecule type: DNA
A;Residues: 1-50,'G',52-1374 <KOG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, A; Reference number: S73101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-1374 <SAK>
A;Cross-references: EMBL:D63426
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J. Mol. Biol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: let-23; CESP: ZK1067.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: strain N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            316
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Biol. 256, 548-555, 1996
                                                                                                        VCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLHNQEVTAEDGTQRCEKCSKPCAR
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                                                              LCSGTTNGISRYGTGNI-LEDLETMYRGCRRVYGNLEITWIEANEIKKWRESTNSTVDPK
                                                                                                                                                                         Similarity
                                                                                                                                                                         18.3%;
29.0%;
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                                                                                                                                                                         Score 419; DB 2;
Pred. No. 4.8e-21;
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A; Residues: 1-1369 <
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                                        SCYTACPYNYLSTDVGSCTLVCPLHNQEVTAEDGT---QRCEKC-SKPCARGTHSLLPRP 349
HCVKECPPELLIXND-----VCVRHCSEGHHYDATKDMRECEKCPSSGC---
                                                                                    ECCDSSCLGGCTNHGPDSCIACSKYEMDEMCIDTCPARKIFNHKTGRLVPNPDGRYQNGN 362
                                                                                                                              DCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGA
                                                                                                                                                                                                   IDTNRSRACHPCSPM------CKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPT---
                                                                                                                                                                                                                                                                                                                                             IDYLKTVNFFDHLEEIRGSLIIYRANIQKISFPKLRVIYGDEVFHDN-SLYIHQNEK---
                                                                                                                                                                                                                                                                                                                                                                                     ----ASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLN 124
                                                                                                                                                                         -XXNSHKACWXNGELIASXHENCK-DKCWGKGDNDCQKIYRSVCPKPCSQCFYSNITQSY
                                                                                                                                                                                                                                                                                                 NTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDT-ILWKDIFHKNNQLALTL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      al Similarity
105; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                           -VNELVMKELRVIRNGSVSIQNNPRMCFLATKVDWNEILYDXSRQKVE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 416; DB 2;
Pred. No. 7.7e-21
59; Mismatches 13
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Length 1369; Indels

68;

Gaps

13

83

197

409

293 302

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protein-tyrosine kinase let-23 precursor homolog - N; Alternate names: receptor tyrosine kinase let-23 C; Species: Caenorhabditis vulgaris c; Date: 21-Apr-1997 #sequence_revision 09-May-1997 C; Accession: $70713
                                                   A:Introns: 42/1; 49/1; 83/1; 105/3; 155/3; 207/1; 280/1; 369/1; 408/1; 438/2; 555/1; C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom C;Keywords: ATP; phosphotransferase; transmembrane protein; tyrosine-specific protein F;1-28/Domain: signal sequence #status predicted <SIG>F;29-1369/Product: protein-tyrosine kinase let-23 homolog #status predicted <MAT>F;929-1194/Domain: protein kinase homology <KIN>F;929-1194/Domain: protein kinase homology <KIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R:Sakai, T.; Koga, M.; Ohshima, Y.
J. Mol. Biol. 256, 548-555, 1996
A;Title: Genomic structure and 5' regulatory
A;Reference number: S70712; MUID:96177760
A;Accession: S70713
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Db Qy 350 AAVPVPL 356 | | | 410 CTVDGPL 416

Search completed: April 11, 2002, 09:30:11 Job time: 108 sec



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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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Query Match
Best Local Similarity
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InterPro; iPR000719; Euk_pkinase.
InterPro; iPR0012174; Furin-like.
InterPro; iPR001245; Tyr_kin.
Pfam; PF00757; Furin-like; 1.
Pfam; PF00069; pkinase; 1.
Pfam; PF01030; Recep_L_domain; 2.
SMART; SM00261; FU; 3.
SMART; SM00261; FU; 3.
SMART; SM00219; TyrKC; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
                                              CONFLICT
SEQUENCE
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NP_BIND
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Transferase; Tyrosine-protein kinase; A
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RESIDUES (BY SIMILARITY).

POLYMORPHISM: THERE ARE FOURS ALLELES DUE TO THE VARIATIONS IN POSITIONS 654 AND 655. ALLELE B1 (654 - ILE-ILE-655) HAS A FREQUENCY OF 0.782; ALLELE B2 (654 - ILE-VAL-655) HAS A FREQUENCY OF 0.206; ALLELE B3 (654 - VAL-VAL-655) HAS A FREQUENCY OF 0.012.

SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M11767; AAA35808.1;
M11761; AAA35808.1;
M11762; AAA35808.1;
M11763; AAA35808.1;
M11764; AAA35808.1;
M11765; AAA35808.1;
M11765; AAA35808.1;
M11765; AAA35808.1;
M11765; AAA35808.1;
M11765; AAA35808.1;
M11769; AAA35808.1;
M11790; AAA35908.1;
M12036; AAA35978.1;
M12036; AAA35978.1;
M12036; AAA35978.1;
M12036; AAA35978.1;
M12036; AAA35978.1;
A25491; A25491.
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A24571;
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I -> V
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CYTOPLASMIC
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RECEPTOR PROTEIN-TYROSINE
EXTRACELLULAR (POTENTIAL).
                                             /FTId=VAR_004078.
P -> A (IN REF. 2).
W; 39E9DFDA04DCF962
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PHOSPHORYLATION (AUTO-)
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ne family; Rece
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-) (BY SIMILAR)
-(POTENTIAL)
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01-JAN-1988 (Rel. 06, Created)
15-DEC-1998 (Rel. 37, Last sequence
20-AUG-2001 (Rel. 40, Last annotati
ERBB-2 RECEPTOR PROTEIN-TYROSINE KI
(P185ERBB2) (NEU PROTO-ONCOGENE) (F
RELATED PROTEIN).
       STRUCTURE BY NMR OF 650-668.
MEDLLNE=92155181; PubMed=1346763;
MULLICK W.J., Bottomley A.C., Lofts F.J., Doak D.G.,
Gullick W.J., Bottomley A.C., Lofts F.J., Campbell
Newman R., Crumpton M.J., Sternberg M.J.E., Campbell
"Three dimensional structure of the transmembrane res
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                                                                                                                          MEDLINE=91222560;
                                                                                                                                     TISSUE=Sciatic
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                                                                                                                                                                                                                   TISSUE=Neuroblastoma;
MEDLINE=86118662; PubMed=3945311;
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NCBI_TaxID=10116;
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                                                                  C., Lemke G.; extended family of protein-tyrosine kinase extended in the vertebrate nervous system."; con 6:691-704(1991).
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oncogenic
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                                                                                                                                      nerve;
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                                                                                                                           PubMed=2025425;
                                                                                                                                                                                              encodes an
                                                                                                                                                                                                                                                                                                  (Rat)
                                                                                                                                                                                                                                                                           Chordata;
Rodentia;
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Last annotation update)
Last annotation update)
IN-TYROSINE KIMASE PRECURSOR (EC 2.7.
O-ONCOGENE) (EPIDERMAL GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      419
forms of the
                                                                                                                                                                                                        Weinberg R.A.;
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                                                                                                                                                                                             epidermal
                                                                                                                                                                                                                                                                          Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                             growth factor receptor-related
                                                                                                                                                                                                                                                                            Muridae;
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                                                                                                   genes
         region
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                                                                                                                                                                                                                                                                            Euteleostomi;
; Murinae; Rat
                   Mulvey
                                                                                                    differentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPVSVGRGPD
            of
                                                                                                                                                                                                                                                                                                                                  RECEPTOR-
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          proto-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180
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Best Local (
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002174; Furin-like.
InterPro; IPR001245; Tyr_kin.
Pfam; PF00757; Furin-like; 1.
Pfam; PF00069; pkinase; 1.
Pfam; PF01030; Recep_L_domain; 2.
SMART; SM00261; FU; 3.
SMART; SM00219; TyrKc; 1.
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SEQUENCE
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PROSITE;
PROSITE;
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THE CONSTITUTIVELY ACTIVATED ONCOGENIC VARIANT SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALPHA AND AMPHIREGULIN.

CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O J. 11:43-48(1992).

FUNCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR COMPLEX, ALTHOUGHT NEUREGULINS DO NOT INTERACT WITH IT ALONE. GP30 IS A POTENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF, TGF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN TYROSINE PHOSPHATE.
SUBUNIT: HETERODIMER WITH EACH OF THE OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESIDUES (BY SIMILARITY)
                                                   A24562;
                  ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a sen the Swiss Institute of Bioinformatics and the EMBI
P11362;
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                                                                                                                                                Similarity
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PS00109;
PS50011;
                                                                                                                               Conservative
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22 1257
22 654
55 677
78 1257
79 369
3 646
2 989
9 736
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1141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN_KINASE_ATP; 1.
PROTEIN_KINASE_TYR; 1.
PROTEIN_KINASE_DOM; 1.
                                                                                                                                                70.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mutation
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ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.

PHOSPHORYLATION (AUTO-) (I

PHOSPHORYLATION (AUTO-) (I

N-LINKED (GLCNAC...) (P

N-LINKED (GLCNAC...) (F

N-LINKED (GLCNAC.
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                                                                                                                                                               Score
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e family; Receptor; Signal;
ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     There are no rest
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CRC64;
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-) (BY SIMILARITY).
) (POTENTIAL).
) (POTENTIAL).
) (POTENTIAL).
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                                                                                                                                                                                                                                                        (POTENTIAL)
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                                                                                                                           1:
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SMART;

Pfam; PF00757; Furin-like; 1.
Pfam; PF00069; pkinase; 1.
Pfam; PF01030; Recep_L_domain

; pkinase; 1.
; Recep_L_domain;
1; FU; 3.
9; TyrKc; 1.

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RESULT 3
ERB2_MESAU
EMBL; D16295; I
InterPro; IPRO
InterPro; IPRO
InterPro; IPRO
InterPro; IPRO
                                                                                                                                                                                                                between
the Euro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q60553;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ERBB-2 RECEPTOR PROTEIN-TYROSINE KINASE PRECURSOR (EC 2.7.1.112)
                                                                                                                                                                                                                                                            This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakamura
Yamazaki
                                                                                                                                  or send
                                                                                                                                                      entities
                                                                                                                                                                        modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mesocricetus auratus (Golden hamster).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (P185ERBB2) (NEU PROTO-ONCOGENE). ERBB2 OR NEU.
                                                                                                                                                                                                                                                                                                                                                                                                            <del>:</del>
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MEDLINE=94193007;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mesocricetus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning
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                                                                                                                                                  s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restr by non-profit institutions as long as its content ified and this statement is not removed. Usage by and ities requires a license agreement (See http://www.isb-sities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALPHA AND CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amura T., Ushijima T., Ishizaka Y., Nagao M., Arai M., azaki Y., Ishikawa T.; oning and activation of the Syrian hamster neu proto-oncogene."; e140:251-255(1994). e140:251-255(1994). e70NCTION: ESSENTIAL COMPONENT OF A NEUREGULIN-RECEPTOR COMPLEX, ALTHOGGHT NEUREGULINS DO NOT INTERACT WITH IT ALONE. GP30 IS A POTENTIAL LIGAND FOR THIS RECEPTOR. NOT ACTIVATED BY EGF, TGF-
                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: HETERODIMER WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN TYROSINE PHOSPHATE
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                                                                                                                                  an
                                                                                                                                                                                                                                                                                                                                              LIGAND-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FROM
  IPR000494; EGFR_L.
IPR000719; Euk_pkinase.
IPR002174; Furin-like.
IPR001245; Tyr_kin.
                                                                                                                                email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIGAND FOR THIS RECEPTOR. NOT ACTIVATED AMPHIREGULIN (BY SIMILARITY).
ACTIVITY: ATP + A PROTEIN TYROSINE = AD
                                                                                        BAA03801.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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PROTEIN_KINASE_ATP;

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Best Local
       01-JAN-1990 (Rel.
01-JAN-1990 (Rel.
20-AUG-2001 (Rel.
EPIDERMAL GROWTH )
                                                  EGFR_CHICK P13387;
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                                                                                                                  IQEFAGCKKIFGSLAFLPESFD---GNPSSGIAPLTPEQLQV 399
                                                                                                                                                                                                                                               PVDIDTNRSRACPPCAPACKDNHCWGASPEDCQTLTGTIAPRAVPAARARLPTDCCHEQC
                                                                                                                                                                                                                                                           LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC
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                                                                                                                                                                                                                                                                                                                                                                                        MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
                                                                                                                                     LRMQPG--PAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPI
                                                                                                                                                                        YNYLSTDYGSCTLYCPLHNQEYTAEDGTQRCEKCSKPCAR-----GTHSLLPRPAAVPVP
                                                                                                                                                                                                      AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTTCP
                                                                                                                                                                                                                 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP
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                                                                                                                                                                                                                                                                                                            DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA
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                                                                                                                                                           YNYLSTEVGSCTLVCPLNNQEVTAEDGTQRCEKCSKSCARVCYGLGMEHLRGARAITSAN
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PS00109;
PS50011;
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                   (Rel. (Rel. (Rel.
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                                                              STANDARD;
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PROTEIN_KINASE_DOM; 1.
PROTEIN_KINASE_DOM; 1.
ycoprotein; Multigene family; Rece
sine-protein kinase; ATP-binding;
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74.48;
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Last annotation updat
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          RECEPTOR
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ERBB-2 REC
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N-LINKED (GLCNAC...
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       PRECURSOR (F
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> E (IN ONCOGENIC NEU).
974C3791C21F2BE1 CRC64;
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No. 3
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nes 67;
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          2.7.
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ing; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1254;
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Ullrich A., Vennstrom B., Schlessinger J., Givol D.; "Chicken epidermal growth factor (EGF) receptor: cDN expression in mouse cells, and differential binding transforming growth factor alpha."; Mol. Cell. Biol. 8:1970-1978(1988).
    CARBOHYD
NON_TER
SEQUENCE
                                                                                                                                                                                           TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Archosauria; Aves; Neognathae; Galliformes; Phasian
                                                                                                                                                                                                                                                                                                          PROSITE; PROSITE;
                                                                                                                                                                                                                                                                                                                                     Pfam; PF00757; Furin-like; 1.
Pfam; PF01030; Recep_L_domain;
SMART; SM00261; FU; 4.
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                                                                                        CARBOHYD
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                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified
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                                            CARBOHYD
                                                             CARBOHYD
                                                                          CARBOHYD
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                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between
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                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000494; EGFR_L.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002174; Furin-like.
InterPro; IPR001245; Tyr_kin.
                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M20386; AAA48760.1; -.
                                                                                                                                                                                                                                                                 Tyrosine-protein
                                                                                                                                                                                                                                                                               !ransmembrane;
                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN TYROSINE PHOSPHATE.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
MISCELLANDOUS: BINDING OF EGF TO THE RECEPTOR LEADS TO
INTERNALIZATION OF THE EGF-RECEPTOR COMPLEX, INDUCTION
TYROSINE KINASE ACTIVITY, STIMULATION OF CELL DNA SYNTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL SIGNAL AND ALSO OF TGF-ALPHA, AMPHIREGULIN, HEPARIN-BINDING EGF, VACCINIA VIRUS GROWTH FACTOR (BY SIMILARITY).

CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a copyright the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                            PS00109;
PS50011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              non-profit institutions as long and this statement is not removed.
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    703
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                                                                                                                                                                                                                                                                                Glycoprotein;
>703
654
667
>703
1134
1190
200
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613
578
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703
                                                                                                                                                                                                                                                                            PROTEIN_KINASE_ATP; PA
; PROTEIN_KINASE_TYR; PA
; PROTEIN_KINASE_DOM; PA
;) PROTEIN_KINASE_DOM; PA
                                                                                                                                                                                                                                                                 kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=3260329;
                                                                                                                                                                                                                                                                 ATP-binding;
    MW;
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N-LINKED
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N-LINKED
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CYTOPLASMIC (POTENTIAL)
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    AFF2DE11B735A690
                             GLCNAC.
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                                                                                                                                                                                                                                                                 Phosphorylation.
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                                                                                                                                                                             (GLCNAC.
                                                                                                                                                                                                                                      GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.isb-sib
                                                                                                                                                                                                                       (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                      FACTOR RECEPTOR.
                                                                                                                                                                                                                                                                               Transferase;
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    CRC64;
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ing of EGF and
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(POTENTIAL).
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RWGLLLALLPPGAA-----STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLE 61

Matches Query Match Best Local :

Similarity

34.8%; 45.5%;

Conservative

55;

Score 796.5; Pred. No. 6.3e 55; Mismatches

.3e-55;

Indels Length

19;

Gaps

7;

DВ

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RESULT 5
EGFR_HMAN
IDFR_CONT 101-101
DT 01-101
DT 01-101
DT 01-100
DE EPIDER 0
OS Homo s
OC Eukary
OC Manmal
OX NCBI_T
RN GIJ
RN MEDLIN
RA MAYES
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                                                                                                                                                                                                                                                                               SEQUENCE OF 150-962 FROM N.A.
MEDLINE=84245835; PubMed=630563;
Xu Y., Ishii S., Clark A.JI., Sullivan M., Wils
Xu Y. Merlino G.T., Pastan I;
"Human epidermal growth factor receptor cDNA is
variety of RNAs overproduced in A431 carcinoma c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 713-924 FROM N.A.
MEDLINE-84196372; PubMed-65261;
Lin C.R., Chen W.S., Kruiger W., Stolarsky L.S., Weber W.,
Evans R.M., Verma I.M., Gill G.N., Rosenfeld M.G.;
"Expression cloning of human EGF receptor complementary DNA:
amplification and three related messenger RNA products in A43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDILINE=84219729; PubMed=6328312; Ulli'ch A., Coussens L., Hayfik J.S., Dull T.J., Gray A., Tam A.V. Lee J., Yarden Y., Libermann T.A., Schlessinger J., Downward J., Mayes E.L.V., Whittle N., Waterfield M.D., Seeburg P.H.; "Human epidermal growth factor receptor cDNA sequence and aberrant expression of the amplified gene in A431 epidermoid carcinoma cells Nature 309:418-425(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMAN STANDARD; PRT; 1210 AA.

P00533; P06268; Q14225;
21-JUL-1986 (Rel. 01, Created)
21-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
EPIDERMAL GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=84219729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                       Biochem.
                                                                                                                                                                              MEDLINE=85046483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science
       SEQUENCE
                                                                            receptor
                                                                                                         "Isolation
                                                                                                                                 O'Malley
                                                                                                                                                                                                                                                          Nature 309:806-810(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cells."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=85270438; PubMed=2991899; Ishii S., Xu Y.H., Stratton R.H., Roe "Characterization and sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Contributory effects of de novo transcription and transcript termination in the regulation of human factor receptor proto-oncogene RNA synthesis."; J. Biol. Chem. 266:1746-1753(1991).
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MEDLINE=91107677;
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"ATP-stimulated interaction
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FUNCTION: THE EGF RECEPTOR MEDIATES AND ALSO OF TGF-ALPHA, AMPHIREGULIN, VACCINIA VIRUS GROWTH FACTOR.
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                                                                                                                                                                                                                                                                                                                                                                         (BY SIMILARITY).
                                                                                                                                                                   793;
No. 2
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                                                                                                                                                                    DB 1;
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                                                                                                                                                                                                                                                                                                                                                       (BY PKC).
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                                                                                                                                                                           Length 1210;
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                                                                                                                                                           Gaps
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RESULT EGFR_MAC O1279
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Eisinger D.P., Serrero G.;

Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL SIGNAL OF I AND ALSO OF TGF-ALPHA, AMPHIREGULIN, HEPARIN-BINDING EGF, GP3/VACCINIA VIRUS GROWTH FACTOR (BY SIMILARITY).

-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE PHOSPHATE.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-!- MISCELLANEOUS: BINDING OF EGF TO THE RECEPTOR LEADS TO INTERNALIZATION OF THE EGF-RECEPTOR COMPLEX, INDUCTION OF THE TYROSINE KINASE ACTIVITY, STIMULATION OF CELL DNA SYNTHESIS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGFR_MOUSE Q01279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=BALB/C, AND CD-1; TISSUE=Liver,
MEDLINE=93126380; PubMed=7678348;
Paria B.C., Das S.K., Andrews G.K., Dey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1996 (Rel.
01-FEB-1996 (Rel.
15-JUL-1999 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=B6/C3; TISSUE=Liver; MEDLINE=94170986; PubMed=8125255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oncogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Avivi A., Skorecki K., Yayon A., Givol D.; "Promoter region of the murine fibroblast growth factor receptor (bek/KGFR) gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BALB/C;
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                                                                                                                                                                                                                                                                                                                                                                                                              Avivi A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Expression of the epidermal growth factor receptor in mouse blastocysts during delayed implantation."; Proc. Natl. Acad. Sci. U.S.A. 90:55-59(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93026370; PubMed=1408137;
                                                                                                                                                                                                                                                                        STRAIN=C3H
                                                                                                                                                                                                                                                                                                                                                              binding site
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91232866; PubMed=2030916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The mouse waved-2 phenotype receptor tyrosine kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Luetteke N.C., Phillips
Jenkins N.A., Lee D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                   Comparison of EGF
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; TISSUE-Liver;
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Sciurognathi; Muridae;
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CELL PROLIFERATION.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.

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                                                                                                                       Query Match
Best Local S
Matches 156
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002174; Furin-like.
InterPro; IPR001245; Tyr_kin.
Pfam; PF00757; Furin-like; 1.
Pfam; PF00050; pkinase; 1.
Pfam; PF010100; Recep_L_domain; 2.
SMART; SM00219; TyrKC; 1.
SMART; SM00219; TyrKC; 1.
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EMBL;
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PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tyrosine-protein SIGNAL 1
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Local Similarity
les 156; Conserv
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L; U03425; AAA17899.1; -.
L; CAA698; CAA42219.1; -.
L; L06864; AAA53029.1; -.
L; Z12608; CAA78249.1; -.
P; P11362; 1FGI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             an email to license@isb-sib.ch).
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                                                          34.5%;
                                                                                                                      134853
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ATP-binding; Phosphorylation;
                                             43;
                                                                                                                               PHOSPHORYLATION (AUTO-
(BY SIMILARITY).

N-LINKED (GLCNAC.

N-LINKED (
                                            Score 789; DB
Pred. No. 4.5e
43; Mismatches
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No. 4.5e-54;
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RESULT 7

ID ERB4_HUMAN STANDARD; PRT; 1308 AA.

ID ERB4_HUMAN STANDARD; PRT; 1308 AA.

AC (15303; AC (15305) 
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                  ALTERNATIVE PRODUCTS: 2 ISOFORMS; JM-A (SHOWN HERE) AND JM-B;
ARE PRODUCED BY ALTERNATIVE SPLICING. THE TWO ISOFORMS DIFFER
FUNCTIONALLY IN THEIR RESPONSE TO PHORBOL ESTER: JM-A IS PROCESSED
BUT NOT JM-B. SO, THEY RESPECTIVELY REPRESENT CLEAVABLE AND
RONCLEAVABLE FORMS OF THE RECEPTOR. BOTH ISOFORMS ARE EXPRESSED IN
CERREBELLUM, BUT ONLY THE JM-B ISOFORM IS EXPRESSED IN THE HEART.
TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN BRAIN, HEART,
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Buropean Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
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Pred. No. 6.1e
45; Mismatches
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ERB3_HUMAN
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ERBB-3 RECEPTOR PROTEIN-TYROSINE KINASE PRECURSOR
(TYROSINE KINASE-TYPE CELL SURPACE RECEPTOR PROTEIN-TYPE CELL SURPACE RECEPTOR PROTEIN-TYPE CELL SURPACE RECEPTOR PROTEIN THE
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P21860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE=90083234; PubMed=2687875;

Kraus M.H., Issing W., Miki T., Popescu N.C., Aaronson S.

"Isolation and characterization of ERBB3, a third member

"Isolation and characterization of ERBB; evidence for ERBB, epidermal growth factor receptor family: evidence for overexpression in a subset of human mammary tumors.";

proc. Natl. Acad. Sci. U.S.A. 86:9193-9197(1989).
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (LONG FORM) AND SECRETED (SHORT FORM).

SECRETED (SHORT FORM).

-!- ALTERNATIVE PRODUCTS: TWO FORMS, A LONG TRANSMEMBRANE FORM AN SHORT SECRETED FORM, EXIST DUE TO ALTERNATIVE SPLICING.

-!- TISSUE SPECIFICITY: EPITHELIAL TISSUES AND BRAIN.

-!- DOMAIN: THE CYTOPLASMIC PART OF THE RECEPTOR MAY INTERACT WITS SH2 OR SH3 DOMAINS OF MANY SIGNAL-TRANSDUCING PROTEINS.

-!- PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE RES AND PROMOTES ITS ASSOCIATION WITH THE PES SUBUNIT OF PHOSPHATIDYLINOSITOL 3-KINASE (BY SIMILARITY).

-!- DISEASE: OVEREXURESSED IN A SUBSET OF HUMAN MAMMARY TUMORS.

-!- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
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                                                                                                                                                                                                                                                     "c-erbB3 gene encodes
tyrosine kinase.";
Biochem. Biophys. Res
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"Molecular cloning and expression factor receptor related gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                              Plowman G.D., Whitney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                  MEDLINE-93282822;
                                                                                                                                                                                                                                                                                                                                 TISSUE=Placenta
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                                                                                                                                                                                SUBUNIT: HETERODIMER (POTENTIAL).
                                                                                                                                                                                                             PROTEIN TYROSINE PHOSPHATE
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Primates;
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Query Match
Best Local Similarity
Matches 150; Conser
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Pfam; PF00069; pkinase; 1.
Pfam; PF01030; Recep_L_domain;
SMART; SM00261; FU; 3.
SMART; SM00219; TyrKC; 1.
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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            NASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTT
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PS00109;
PS50011;
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IPR000719; Euk_pkinase.
IPR002174; Furin-like.
IPR001245; Tyr_kin.
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; PROTEIN_KINASE_TYR; FA
; PROTEIN_KINASE_DOM; 1
;lycoprotein; Multigene f
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560
1064
A; 148097
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N-LINKED (GLCNA
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E -> G (IN REF. 2).
E -> G (IN REF. 2).
MW; 7201E7F66CA374BD CRC64;
                                                                                                                                                               Score 735.5;
Pred. No. 7.7e
19; Mismatches
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VPVTLAAV
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EILSGGVYIEKNDKLCHMDTIDWRDIVRDRDAEIVVKDNGR
SC -> GOFPMVPSGLTPQPAQDWYLLDDDPRLLTLSASSK
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No. 7.7e-50;
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ne family; Rece
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or send a
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the Euro
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J. Neurosci. 17:1642-1659(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q62799; Q62955;
15-DEC-1998 (Rel. 37, Created)
15-JUL-1999 (Rel. 38, Last sequer
15-JUL-1999 (Rel. 38, Last annote
ERBB-3 RECEPTOR PROTEIN-TYROSINE
           InterPro;
InterPro;
                                    EMBL; U29339; AAC28498.1; -. EMBL; U52530; AAC53050.1; -.
                                                                                                             use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hellyer N.J., Kim H.-H., G
"Cloning of the rat ErbB3
recombinant protein.";
Gene 165:279-284(1995).
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                                                                                                modified
                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97184212; PubMed=9030624;
Carroll S.L., Miller M.L., Frohne
                                                                                                                                                                                                                                                                                                                                                                                                                         Hellyer N.J
Submitted (
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Mammalia; I
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                                                                                                                    s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no rest
                                                                                                                                                                                               SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
DOMAIN: THE CYTOPLASMIC PART OF THE RECEPTOR MAY INTERACT
SH2 OR SH3 DOMAINS OF MANY SIGNAL-TRANSDUCING PROTEINS.
PTM: LIGAND-BINDING INCREASES PHOSPHORYLATION ON TYROSINE
AND PROMOTES ITS ASSOCIATION WITH THE P85 SUBUNIT OF
                                                                                                                                                                                                                                                                                                 FUNCTION: BINDS AND IS ACTIVATED BY CATALYTIC ACTIVITY: ATP + A PROTEIN
                                                                                                                                                                        SIMILARITY: BELONGS TO THE EGF RECEPTOR
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ipr000719; |
ipr002174; |
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                                                                        email to license@isb-sib.ch)
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oa; Chordata;
ia; Rodentia;
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PubMed=8522190;
H.-H., Greaves C.H
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tors, ErbB2
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RESULT 10

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PROSITE; PS00109; PROTEIN_KINASE_TYR; I
PROSITE; PS50011; PROTEIN_KINASE_DOM; I
Transmembrane; Glycoprotein; Multigene
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47; Conservative
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Recep_L_doma
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R PROTEIN-TYROSINE F
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR001145; Tyr.kin.
Pfam; PF001245; Tyr.kin.
Pfam; PF00757; Furin-like; 1.
Pfam; PF001030; Recep_L_domain; 2.
Pfam; PF001030; Recep_L_domain; 2.
SMART; SM00219; TyrKc; 1.
PROSITE; PS001109; PROTEIN_KINASE_N; PROSITE; PS00109; PROTEIN_KINASE_T)
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Eukaryota; Metazoa; Chordata; Cranlata; Puttebrata; Euteleos
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neotele
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha
Cyprinodontiformes; Poeciliidae; Xiphophorus.
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Wittbrodt J., Adam D., Malitschek B.,
Telling A., Robertson S.M., Schartl M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACLIVIANCE PROTEIN TYROSINE PROTEIN TYROSINE PROTEIN. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. DISEASE: INVOLVED IN PIGMENT CELLS MALIGNANT MEDISEASE: RECEPTOR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
FUNCTION: PROBABLE RECEPTOR WITH PROTEIN-TYROSINE KINASE
CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
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Similarity

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C P04412; 061601, 299730; P81868;

T 13-AUG-1987 (Rel. 05, Created)

T 15-DEC-1998 (Rel. 37, Last sequence update)

T 20-AUG-2001 (Rel. 40, Last annotation update)

E EPIDERMAL GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (EC GURKEN RECEPTOR) (TORPEDO PROTEIN) (DROSOPHILA RELATIVE OF E (GURKEN RECEPTOR) CORDER OR CG10079.

N EGFR OR TOP OR C-ERBB OR DER OR CG10079.

SEGFR OR TOP OR C-ERBB OR DER OR CG10079.

C EURALYOLIA Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Curary Tracheata; Drosophila melanogaster (Fruit fly).

C Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc Pterygota; Drosophilia.
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Matches
                         Schejter E.D., Segal D., Glazer L., Shilo B.-Z.;
"Alternative 5' exons and tissue-specific expression
Drosophila EGF receptor homolog transcripts.";
Cell 46:1091-1101(1986).
                                                                                                                                                                      "The
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                                                                                                                                                                                              MEDLINE=85124611;
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Molecular analysis of the Drosophila EGF
that several genetically defined classes
subdomains of the receptor protein.";
Genetics 137:531-550(1994).
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Drosophila EGF receptor gene Pone binding and kinase domains
40:599-607(1985).
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RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Addams M.D., Celniker S.E., Holt R.A.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
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RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aphayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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RA Codson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywan C.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Kulp D., Lai Z.,
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RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Ralazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Ralazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Ralazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Ralazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
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RA Shue B. C., Siden-Klamos I., Sinpson M., Skupski M.P., Smith T.,
RA Ralazolo M., Reinny G., Stappson M., Skupski M.P., Smith T.,
RA Ralazolo M., Reinny G.,
                  Perrimon N., Per
"There must be "
EGF receptor.";
Cell 89:13-16(1997).

Cell 89:13-16(1997).

-I- FUNCTION: BINDS TO FOUR LIGANDS: SPITZ, GURKEN, VEIN AND ARGOS, WHICH IS AN ANTAGONIST. TRANSDUCES THE SIGNAL THROUGH THE RAS-F MAPK PATHWAY. INVOLVED IN A MYRIAD OF DEVELOPMENTAL DECISIONS.

MAPK PATHWAY. TOR THE PROLIFERATION OF IMAGINAL TISSUES, AND FOR THE
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of EGF receptor signaling during photoreceptor
wild-type, Ellipse, and null mutant Drosophila.";
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Pfam; PF00757; Furin-like; 1.
Pfam; PF00069; pkinase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -
                                                                     Transmembrane; Glycoprotein; Tyrosine-protein kinase; ATP
                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P11362; 1FGI.
FlyBase; FBgn0003731; Egfr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This
                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                     [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED IN EMBRYOS. IN LARVAE, UNIFORM EXPRESSION IS SEEN IN WING DISKS, GENITAL DISK, ANLAGEN OF TESTIS AND OVARY, AND BRAIN CORPEX. IN EYE-ANTENNA DISK, HIGHEST EXPRESSION IS ANTERIOR TO MORPHOGENETIC FURROW, LEVELS REMAIN HIGH IN PHOTORECEPTOR PRECURSOR CELLS. THIS PATTERN IS REVERSED IN POSTERIOR EYE DISK. IN ADULTS EXPRESSION IS HIGH IN BRAIN CORTEX AND THORACIC AND ABDOMINAL GANGLIA.

SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CUTICLE.
CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE =
PROTEIN TYROSINE PHOSPHATE.
SUBCELLULAR LOCATION: ISOFORMS TYPE I AND TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF052754; AAC08536.1;
AF052754; AAC08535.1;
AF052752; AAC08535.1;
K03054; AAA51460.1;
K03417; AAA51460.1;
K03418; AAA50965.1;
K03418; AAA50965.1;
AF109078; AAD26132.1;
AF109078; AAD26132.1;
AF109084; AAD26132.1;
AF109084; AAD26133.1;
AF109079; AAD26133.1;
AF109079; AAD26133.1;
AF109079; AAD26133.1;
AF109081; AAD26130.1;
AF109080; AAD26131.1;
AF109080; AAD26131.1;
AF109080; AAD26131.1;
AF109080; AAD26131.1;
AF109080; AAD26131.1;
AF109080; AAD26135.1;
AF109080; AAD26135.1;
AF109080; AAD26135.1;
AF109080; CAA55523.1;
AF109080; CAA55523.1;
AF109080; CAA55522.1;
AF109080; CAA55522.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALTERNATIVE PRODUCTS: 3 ISOFORMS; TYPE I (SHOWN HERE), TYPE III; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DETERMINATION OF BOTH THE ANTERO-POSTERIOR AND DORSO-VENTRAL POLARITIES OF THE COCYTE. IN THE EMSTRYO, PLAYS A ROLE IN THE ESTABLISHMENT OF VENTRAL CELL FATES, MAINTENANCE OF AMNIOSEROSA AND VENTRAL NEUROECTODERMAL CELLS, GERM BAND RETRACTION, CELL FASECLIFICATION IN THE CENTRAL NERVOUS SYSTEM AND PRODUCTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEMBRANE PROTEINS. ISOFORM TYPE
                                                 opmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A00640; GQFFE.
                                                           PS00107; PROTEIN_KINASE_ATP; 1.
PS00109; PROTEIN_KINASE_TYR; 1.
PS50011; PROTEIN_KINASE_DOM; 1.
PS50011; PROTEIN_KINASE_DOM; 1.
PS50011; PROTEIN; Receptor; Phosphorylation; Tr
brane; Glycoprotein; Receptor; Signal; Alternative
                                                                                                                                                                                                                                                                                                            IPR000494; EGFR_L.
IPR000719; Euk_pkinase.
IPR002174; Furin-like.
IPR001245; Tyr_kin.
                                         protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOINED.
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POTENTIAL.
EPIDERMAL
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GROWTH FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      I AND TYPE III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                restrictions
                                                                                           Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . IN LARVAE,
                                                                     splicing;
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RESULT 12
LT23_CAEEL
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Best Local S
Matches 118
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CARBOHYD
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BINDING
ACT_SITE
MOD_RES
MOD_RES
                    [3]
                                                                                                        Nature
[2]
                                                                                                              MEDLINE=91080919; PubMed=1979659; Aroian R.V., Koga M., Mendel J.E., Ohshima Y., "The let-23 gene necessary for Caenorhabditis induction encodes a tyrosine kinase of the EGF Nature 348:693-699(1990).
                                                                                                                                                                                                                                  U1-MAR-1992 (Rel. 21, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
LET-23 RECEPTOR PROTEIN TYROSINE KINASE PRECURSOR
LET-23 OR KIN-7 OR ZK1067.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                             STRAIN=BRISTOL N2;
MEDLINE=96177760; PubMed=8604137;
Sakai T., Koga M., Ohshima Y.;
                                                                                                                                                                                                      Caenorhabditis elegans
Eukaryota; Metazoa; Nen
Rhabditidae; Peloderina
                                                                                                                                                                                                                                                         01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last seg
20-AUG-2001 (Rel. 40, Last ann
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                                         the
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           SEQUENCE
                                                     "Genomic
                                                                                                                                                                        SEQUENCE FROM
                                                                                                                                                                                            NCBI_TaxID=6239;
                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                         382
                                                                                                                                                                                                                                                                                                                                                                                                 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24
                                Mol.
                               nematode C. elegans.";
Mol. Biol. 256:548-555(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPT-NASLSFLQDIQEVQG
                                                                                                                                                                                                                                                                                                    CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                YVLIAHNQVRQVPLQRLRIVRGTQLF----EDNYALAVLDNGDPLNNTTPVTGASPGGL 137
                                                                                                                                                                                                                                                                                                                                                                                                                                         YTLEIPDLRDVLNGQVGFHNNYNLCHMRTIQWSEIVSNGTDAYYNYDFTAPERECPKCHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNRSRACHPCSP 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 al Similarity
118; Conserv
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                                                                                                                                                                                                                                                                                                                                                                             PLHNQEVTAEDGTQRCEKCSKPCAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MCKGSRCWGESSEDCQSLTRTVCAGGCA--RCKGPLPTDCCHEQCAAGCTGPKHSDCLAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YILISHVDVKKVVFPKLQIIRGRTLFSLSVEEEKYALFV
                                                  , Koga M., Ohshima Y.; structure and 5' regulatory regions
           FROM
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971
1063
902
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241
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                                                                                                                                                                                                     Peloderinae;
          N.A.
                                                                                                                                                                        N.A.
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889
1426
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128
                                                                                                                                                                                                       Nematoda; Chromadorea; cinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.1%;
36.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 574.5; DB 1;
Pred. No. 3.2e-37;
6; Mismatches 130;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED
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POTENTIAL.
                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                   Ohshima Y.,
                                                                                                                                                                                                                                                                                                    1323
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                                                                                                                               EGF
                                                                                                                                                                                                                  Rhabditida; Rhabditoidea
                                                     of.
                                                                                                                                          elegans
                                                                                                                            receptor subfamily.";
                                                                                                                                                   Sternberg P.W.;
                                                     the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                (EC 2.7.1.112).
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                                                     let-23
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                                                                                                                                          vulval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1426;
                                                    gene
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                                                     in
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VARIANT
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                                                                                                                          VARIANT VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00757; Furin-like; 1.
Pfam; PF00069; pkinase; 1.
Pfam; PF01030; Recep_L_domain;
SMART; SM00261; FU; 6.
SMART; SM00219; TYXKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X57767; CAA40919.1; ALT_SEQ
EMBL; D63426; BAA09729.1; ALT_INIT
EMBL, Z70038; CAA93882.1; -.
PIR; S13422; S13422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000494; EGFR_L.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002174; Furin-like.
InterPro; IPR001245; Tyr_kin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WormPep; ZK1067.1: 'InterPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. The Theorem The Transfer of the Transfe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         elements
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"Mutations in the Caenorhabditis elegans let-23 EGFR-like gene define elements important for cell-type specificity and function.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aroian R.V.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALITIC ACTIVITY: ATP + A PROTEIN TYROSINE = PROTEIN TYROSINE POSPHATE.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: TYROSINE KINASE RECEPTOR REQUIRED FOR THE INDUC
C.ELEGANS VULVA. POSSIBLE RECEPTOR FOR THE INDUCTIVE SIGN
REQUIRED FOR VULVAL DEVELOPMENT. ACTIVATED BY LIN-3 AND &
WAY OF LET-60 RAS. THE LIN-3/LET-23 PAIR IS A SIMPLIFIED
OF THE MAMMALIAN NEUREGULIN-ERBB NETWORK.
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PROTEIN_KINASE_TYR;
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SIMILARITY)
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Best Local Similarity
Matches 102; Conser
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
INSULIN-LIKE PEPTIDE RECEPTOR PRECURSOR (EC 2.7.1.112) (ILP RECEPTOR).
Branchiostoma lanceolatum (Common lancelet) (Amphioxus).
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=96408719; PubMed=8813726;
Pashmforoush M., Chan S.J., Steiner D.F.;
"Structure and expression of the insulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae; Branchiostoma. NCBI_TaxID-7740;
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                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                HAS A TYROSINE-PROTEIN KINASE ACTIVITY CATALYTIC ACTIVITY: ATP + A PROTEIN TYPEROTEIN TYROSINE PHOSPHATE.
SUBUNIT: PROBABLE TETRAMER OF 2 ALPHA &
                                                                                                                                                                                                           THE LIGAND-BINDING DOMAIN, WHILE THE BETA CHAIN CARRY THE KINDOMAIN (BY SIMILARITY).
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE
                                                                                                                                                                                                                                                                                                                                           FUNCTION: THIS
                                                                                                                                                                                               PROTEIN KINASES.
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SMART; SM00060; FN3; 3.
SMART; SM00261; FU; 1.
SMART; SM00219; TYFKC; 1.
PROSITE; PS00107; PROTEIN_K
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SIGNAL
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PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
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PF00757;
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 RTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCLACLHENHSGICELHCPALVTYNT
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                                  IDWSFIAESGYSNN----FIVDNREEEECVNFCPGRCRIKHPVLQDLCWAE--EHCQKVC
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F01030; Recep_L_domain;
PR00014; FNTYPEIII.
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IPR001245; Tyr_kin.
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INSR_DROME
                                                                                                                     domain of the human insulin receptor and detection of the phosphorylated Drosophila receptor with an anti-peptide antibody."; proc. Natl. Acad. Sci. U.S.A. 83:4710-4714(1986).

Proc. Natl. Acad. Sci. U.S.A. 83:4710-4714(1986).

Proc. Natl. Acad. Sci. U.S.A. 83:4710-4714(1986).

Proc. Natl. Receptor Probably BINDS AN INSULIN RELATED PROTEIN AND HAS A TYROSINE-PROTEIN KINASE ACTIVITY (BY SIMILARITY).

PROTEIN TYROSINE PHOSPHATE.

PROTEIN TYROSINE PHOSPHATE.

SUBUNIT: TETRAMER OF 2 ALPHA AND 2 BETA CHAINS LINKED BY DISULFIDE BONDS. THE ALPHA CHAINS CONTRIBUTE TO THE FORMATION OF THE LICAND-BINDING DOMAIN, WHILE THE BETA CHAIN CARRY THE KINASE DOMAIN.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
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signaling potential.";
EMBO J. 14:3373-3384(1995).
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Eukaryota; Metazoa; Arthropoda; Tracheata; He
Eukaryota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-OREGON-R; TISSUE-Embryo; MEDLINE-87100165; PubMed-399787; NIShida Y., Hata M., Nishizuka Y., Rutt "Cloning of a Drosophila cDNA encoding human insulin receptor precursor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ruan Y., Chen C., Cao Y., Garofalo R.S.;
"The Drosophila insulin receptor contains a novel carboxyl-terminal extension likely to play an important role in signal transduction.";
J. Biol. Chem. 270:4236-4243(1995).
                This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fernandez R., Tabarini D., Azpiazu N., Frasch M., 
"The Drosophila insulin receptor homolog: a gene embryonic development encodes two receptor isoform
                                                                                                                                                                                                                                                                                                                                         Birnbaum M.J., Rosen O.M.; ^{\circ} Isolation of a Drosophila genomic sequence homologous to the
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Interpro; IPR002011; Rcptor_tyr_kin_II.
Interpro; IPR001245; Tyr_kin.
Pfam; PF00757; Furin-like; 1.
Pfam; PF00069; pkinase; 1.
Pfam; PF01030; Recep_L_domain; 1.
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PROTEIN_KINASE_TYR; 1.
RECEPTOR_TYR_KIN_II; 1.
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31 MKLRLPASPETHLD---MLRHLYQ--GCQVVQGNLELTYL----PTNASLSFLQDIQEVQ
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                                                                                                                                                                                                                                                                                                                          RYTFGASCVTA------CPYNYLSTDVGSCTLVCPLHNQEVTAEDGTQR 330
                                                                                                                                                                                                                                                                                                                                                             --EHTCCSQDCLGGCVIDKNGNESCISCRNVSFNNICMDSC---
                                                                                                                                                                                                                                                                                                                                                                             PLPTDCCHEQCAAGCTGPKHSD--CLACLHFNHSGICELHCPALVTYNTDTFESMPNPEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MRLSQNVKPCKSMDIRNMVSHFNQLENCTVIEGFLLIDLINDASPLNRS---FPKLTEVT 386
                                                                                                                                                                                                                                                                                                                                                                                                                               SKCPGEIRIEEGHDNTAIEGELNASCQLHNNRRLCW--NSKLCQTKCPEKCRNNCID---
Cnidaria; Hydrozoa; Hydroida;
                                              Last sequence update)
Last annotation update)
PEPTIDE RECEPTOR PRECURSOR
                 (Hydra vulgaris).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 294; DB
Pred. No. 4.5e
43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     V -> VTEV (IN REF. 2).

NLMA -> KPYGV (IN REF. 2).

MISSING (IN REF. 3).

LCSDYD -> SAAIIH (IN REF. 3).

ATESLGRHOL -> VRRWTPPV (IN REF. 2).

DFNQTAGYLIKLNEGLYSFR -> RLQPDCRLENKAQRGPL
OLO (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TKRENILÄIPTPESERQEPETDPTCLKRTGCDRRVRQGLHH PMDSSEGRRNRYEL -> SQTRKSPTNPNSGIGATGAGNRS NLLKENW LRPASTPRPP PPNGFIGREA (IN
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GD -> VE (IN REF. 3).
EERDEAMMTYLNRIGV -> PRSGMRPDDVSLIAWM
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.5e-15;
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Query Match
Best Local Similarity
Matches 94; Conser
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Pfam; PF00057; Furin like; 1.
Pfam; PF00069; Pkinase; 1.
Pfam; PF01030; Recep_L_domain; 1
PRINTS; PR00109; TYRKINASE.
SMART; SM00060; FN3; 1.
SMART; SM00261; FU; 1.
SMART; SM00219; TYRK: 1.
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SEQUENCE FROM P
Steele R.E., M
                                              CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M64612; AAA68205.1; -. HSSP; P06213; 1IRK.
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                                                                                                                                                                                                                                                                                                                    PROSITE; PS00107; PROSITE; PS00109;
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                                                                                                                                                                                                                                                                                 Glycoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN KINASES.
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IPR002011; Rcptor tyr_kin_II.
IPR001245; Tyr_kin.
0041; fn3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR000494; EGFR_L.
IPR000719; Euk_pkinase.
IPR001777; FN_III.
                                                                                                                                                                                                                                                    ain; Arp-binding; Phosphorylation; S. 1 Porms Portential. 25 1477 prms 25 1477
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01109; PROTEIN_KINASE_TYR; 1.
0239; RECEPTOR_TYR_KIN_II; 1.
0011; PROTEIN_KINASE_DOM; 1.
Tyrosine-protein_kinase; Receptor; Transmembrane;
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Score 291; DB
Pred. No. 5.1e
34; Mismatches
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PUTATIVE INSULIN-LIKE PEPTIDE RECEPTOR.
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                   Length 1477;
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                                                                                  GICELHCPALVTYNTDTF---ESMP-----NPEGRYTFGASCVTACPYNYLSTDVGSCT
                                                                                                             KQQNKAQCQRFCNTQC--GPEGCLDGSDHICCHHECLGGCSAINSTNTCHACRKYRIKST
                                                                                                                                           --ESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSD-CLACLHF--NHS
                                                                                                                                                                     IRWKSIIKDIHQTGQYGIYL-ESNKLNCDLGCLKGHCHPAPGHDGDP--KAQYCWGPGPK
                                                                                                                                                                                                                                             LFEDNYALAYLDNGDPLNNTTPYTGASPGGLRELQLRSLTEILKGGYLIQRNPQLCYQDT
                                                                                                                                                                                                                                                                                    QNCTCWHGNLVVKSTKYYDEENFKPYFPKLREITGYLLISLCTLKFFHLFPGLTVIRGGD
                                                                                                                                                                                                                                                                                                               QGCQVVQGNL---ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPL-QRLRIVRGTQ
----NNQ-----TKKCEKC 333
                          LVCPLHNQEVTAEDGTQRCEKC
                                                       GQCVSKCPR-KQYLVDKFLCQESCPYWSINSTEYHHYLWQGECVTKCPVNYIS-----
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Search completed: April 11, 2002, 09:34:23 Job time: 310 sec

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Result
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1 MELAALCRWGLLLA
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Compugen Ltd.
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P79754
                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (without alignments)
1515.157 Million cell updates/sec
      0922n7 rattus norv
09ese0 rattus norv
09bud7 homo sapien
09bg66 oryttolagus
09yh40 xiphophorus
p79754 fugu rubbip
p09psh2 gallus gall
                                                                                Q9erv6 mus musc
Q9wvf5 mus musc
Q9ep98 mus musc
Q9qx70 rattus r
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Q9gzx1 homo
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Q92795 homo sapien
Q9h2c9 homo sapien
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O18735 canis famil
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181.5	189	191	203	210	230	232	252.5	270	272	273.5	284	290	294	298	298	298.5	300	331	331	363.5	363.5	395	402.5	404.5	463.5
7.9	8.3	8.4	8.9	9.2	10.1	10.1	11.0	11.8	11.9	12.0	12.4	12.7	12.9	13.0	13.0	13.1	13.1	14.5	14.5	15.9	15.9	17.3	17.6	17.7	20.3
91	131	82	1846	868	946	1245	1371	410	469	89	1362	1300	2144	1418	1358	1671	1472	342	334	1717	366	151	1368	150	1137
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O88458 mus musculu	Q9bh16 anopheles g	Q9n0k4 sus scrofa	Ol6131 caenorhabdi	Q9vfe2 drosophila		scopht		Q63720 rattus norv	Q63721 rattus norv	O88459 mus musculu	Q9pvz4 xenopus lae	Q9wt14 mus musculu	Q9vd94 drosophila	O93457 scophthalmu	073798 xenopus lae	Q9njv5 biomphalari			Q26567 schistosoma		Q26569 schistosoma	Q9bg65 oryctolagus	Q23821 caenorhabdi	Q9bg64 oryctolagus	Q9w6f6 gallus gall

ALIGNMENTS

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                                                                                                        RESULT
Q9UK79
                                             Query Match
Best Local Similarity
Matches 417; Conserv
                                                                                                                                                                                                                                                                                                                                                                                         Q9UK79;
Q9UK79;
Q1-MAY-2000
Q1-MAR-2001
Q1-JUN-2001
                                                                                                      InterPro; IPR000494; EGFR_L.
InterPro; IPR002174; Furin-like.
Pfam; PF00757; Furin-like; 1.
Pfam; PF01030; Recep_L_domain; 1.
SMART; SM00261; FU; 1.
SEQUENCE 419 AA; 45472 MW; FE
                                                                                                                                                                                                                                              Doherty J.K., Clinton G.M., Adelman J.P., Evans A.J., H Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases EMBL; AF177761; AAD56009.2; -.
                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 96:10869-10874(1999)
                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 HERSTATIN
             MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
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                                                Conservative
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                                                                                                        45472 MW; FEC1BE347E2D030C CRC64;
                                                        99.5%;
99.5%;
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16,
                                             Score 2275; DB 4;
Pred. No. 4.9e-190;
1; Mismatches 1;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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61 ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120

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R InterPro; IPR000719; Euk_pkinase.
R InterPro; IPR0002174; Furin-like.
R InterPro; IPR0012145; Tyr_kin.
R InterPro; IPR001245; Tyr_kin.
R Pfam; PF00757; Furin-like; 1.
R Pfam; PF00069; pkinase; 1.
R Pfam; PF00069; pkinase; 1.
R Pfam; PF001030; Recept_domain; 2.
R SMART; SM00261; FU; 3.
R SMART; SM00219; TyrKC; 1.
R SMART; SM00219; TyrKC; 1.
R PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
R PROSITE; PS00117; PROTEIN_KINASE_DOM; 1.
R PROSITE; PS00119; PROTEIN_KINASE_TYR; 1.
R PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
                                                                                                                                                                                                                                                                                     Matches
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Best Local Similarity
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018735;
01-JAN-1998
01-JAN-1998
01-JUN-2001
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Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; (Mammalia; Eutheria; Carnivora; MCBI_TaxID~9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (OCT-1997)
EMBL; AB008451; BAA23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P06213;
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                                                                                    ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG
                                                                                                                                                                      MELAAWCRWGLLLLALLPSGAAGTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
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82.2%;
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Pred. No. 7.3
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Canis.
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Best Local Similarity
Matches 155; Conser
                                                                                                                                                                                                                                    Signal.
SIGNAL
CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q90836 PRELIMINARY; PRT; 527 AA. Q90836; O1-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence up 01-JUN-2001 (TrEMBLrel. 17, Last annotation EGEF/TGF-ALPHA RECEPTOR PRECURSOR. C-ERBB.
                                                                                                                                                                                                                                                                                        InterPro; IPR000494; EGFR_L.
InterPro; IPR002174; Furin-like.
Pfam; PF00757; Furin-like; 1.
Pfam; PF01030; Recep_L_domain; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                      dependent transformation.";
mol. Cell. Biol. 12:883-893(1992).
EMBL; M77637; AAA48759.1; -.
                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-92123214; PubMed=1732751;
Flickinger T.W., Maihle N.J., Kung H.J.;
"An alternatively processed mRNA from the avian of soluble, truncated form of the receptor that can
                                                                                                                                                                                                                                                                                SMART; SM00261; FU;
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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 FASNLSSCPKCHPNCTEDHCWGAGEQNCQTLTKVICAQQCSGRCRGKVPSDCCHNQCAAG
                                                     TTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILMKDIFHKNNQLALTLID
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527
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                                                                                                                                                                                                                                      AA;
                                            -GLRELPMKRLSEILNGGVKISNNPKLCNMDTVLWNDIIDTSRK-PLTVLD
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527
58353 →
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                                                                                                                                                                             Score 794; DB 13;
Pred. No. 5.7e-61;
5; Mismatches 109
                                                                                                                                                                                                                                    POTENTIAL.
EGF/TGF-ALPHA RECEPTOR.
764564ABCC095298 CRC64;
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                                                                                                                               MEDLIND-B5207089, FURNING MEDLIND-B5207089, FURNING S.T., IShii S., Whang-Peng J., Knutsen T., Xu r.-n., Merlino G.T., Ishii S., Whang-Peng J., Knutsen T., Xu r.-n., Clark A.J.L., Stratton R.H., Wilson R.K., Ma D.P., Roe B.A., Hunts J.H., Shimizu N., Pastan I.;

"Structure and localization of genes encoding aberrant and normal structure and localization of genes encoding aberrant and normal structure and localization of genes encoding aberrant and normal structure and localization of genes encoding aberrant and normal structure and localization of genes encoding aberrant and normal structure.
                                                                                                                             epidermal cells.";
                                                                                                                                                                                                                                                                                                                                          Lee J., Yarden Y., Libermann T.A., Schlessinger J., Downward J., Mayes E.L.V., Whittle N., Waterfield M.D., Seeburg P.H.;
"Human epidermal growth factor receptor cDNA sequence and aberrant expression of the amplified gene in A431 epidermoid carcinoma cells Nature 309:418-425(1984).
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  SEQUENCE FROM N.A.
Reiter J.L., Threadgill
Schehl Sinclair C., Pear
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MEDLINE-85267689; PubMed=2991749;
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MEDLINE=84219729; PubMed=6328312;
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Mammalia; Eutheria;
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Motazoa; Chordata;
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01-FEB-1997 (TrEMBLrel.
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EPIDERMAL GROWTH FACTOR
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RECEPTOR PRECURSOR (P60 EPIDERMAL GROWTH
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EMBL; U95089; AAB53063.1; --
EMBL; AF288738; AAG35787.1; --
InterPro; IPR000494; EGFR_L
InterPro; IPR002174; Furin-like.
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SEQUENCE FROM N.A. MEDLINE=84219729;
                                          Eukaryota; Metazoa; Mammalia; Eutheria;
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                                                                 Homo sapiens (Human).
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Redbl., Arcastopoly to the EMBL/GenBank/DDBJ
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ
InterPro; IPR00345; ECFR_L.
InterPro; IPR002174; Furin-like.
Pfam; PF01030; Recep_L_domain; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clark A.J.L., Stratton R.H., Wilson K.A., Wi
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"A 1.8 kb alternative transcript from the factor receptor gene encodes a truncated f Nimoleic acids Res. 24:4050-4056(1996).
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Receptor.
SEQUENCE 628 AA;
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Schehl Sinclair C., Pearall R.S., Green P.J., Yee D., La
Balasubramaniam S., Crossley T.O., Magnuson T.R., James
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MEDLINE-85267689; PubMed-2991749;
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Mayes E.L.V., Whi
"Human epidermal
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RESDCLVCRKFRDEATCKDTCPPLMLYNPTTYQMDVNPEGKYSFGATCVKKCPRNYVVTD
                          KHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTD
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K., Ma D.
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е В.А.,
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Lampland A.L.,
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Merlino G.T., Ishii S., Whang-Peng J., Knutsen
Clark A.J.L., Stratton R.H., Wilson R.K., Ma D.
Hunts J.H., Shinizu N., Pastan I.;
"Structure and localization of genes encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                  Merlino G.T., Ishii S., Whang-Peng J., Knutsen T., Xu Y.-H., Clark A.J.L., Stratton R.H., Wilson R.K., Ma D.P., Roe B.A., Hunts J.H., Shimizu N., Pastan I.; "Structure and localization of genes encoding aberrant and normal epidermal growth factor receptor RNAs from A431 human carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLLINE=84219729; PubMed=6328312;

Ullrich A., Coussens L., Hayflick J.S., Dull T.J., Gray A., Te
Lee J., Yarden Y., Libermann T.A., Schlessinger J., Downward of
Mayes E.L.Y., Whittle N., Waterfield M.D., Seeburg P.H.;

"Human epidermal growth factor receptor cDNA sequence and aber
expression of the amplified gene in A431 epidermoid carcinoma
Nature 309:418-425(1984).
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"A 1.8
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
EPIDERMAL GROWTH FACTOR RECEPTOR (A431-SPECIFIC P115 EPIDERMAL GROWTH
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EMBL; K03193; AAA52371.1;
EMBL; U48728; AAC50800.1;
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Schehl Sinclair C., Pearall R.S., O
Schehl Sinclair S., Crossley T.O.,
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"Comparative genomic
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MEDLINE=85267689; PubMed=2991749;
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.8 kb alternative transcript from
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Green P.J., Yee
, Magnuson T.R.,
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Best Loc
Matches
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O1-MAR-2001 (TrEMBLrel. 16, Cr
O1-MAR-2001 (TrEMBLrel. 17, L
O1-JUN-2001 (TREMBLREL. 17, L
TRUNCATED EPIDERWAL GROWTH FA
                                                                                                                                         "Human and mouse alternative EGFR transcripts extracellular domain of the receptor."; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                              Lampland Maihle N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
InterPro;
Pfam; PF00
Pfam; PF01
                                                                                                                                                                                                                                                      Homo sapiens (Human).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Primates; Catarrhini; Hominidae
                                 Ullrich A., Coussens L., Hayflick J.S., Dull T.J., Gray A., Lee J., Yarden Y., Libermann T.A., Schlessinger J., Downward Mayes E.L.V., Whittle N., Waterfield M.D., Seeburg P.H.; "Human epidermal growth factor receptor cDNA sequence and at expression of the amplified gene in A431 epidermoid carcinon Nature 309:418-425(1984).
                                                                                             MEDLINE=84219729; PubMed=6328312; Ullrich A., Coussens L., Hayflick
                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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SEQUENCE
 MEDLINE=85267689;
            SEQUENCE
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rPro; IPR002174; F
; PF00757; Furin-1; PF01030; Recep_L
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002174; Furin-like.
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 PubMed=2991749;
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FACTOR RECEPTOR PRECURSOR (P110
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Submitted (JUL-2000) to the EMBL/GenBa
EMBL; AF12525; AAG43240.1; -
EMBL; AF288738; AAG35786.1; -
InterPro; IPR000345; Cytc_heme_bind.
InterPro; IPR000494; EGFR_L.
InterPro; IPR002174; Furin-like.
Pfam; PF00757; Furin-like; 1.
Pfam; PF01030; Recep_L_domain; 2.
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SIGNAL
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SEQUENCE
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Clark A.J.L., Stratton R.H., Wilson R.K., Ma D.P., Roe
Hunts J.H., Shimizu N., Pastan I.;
"Structure and localization of genes encoding aberrant
epidermal growth factor receptor RNAs from A431 human of
                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reiter J.L., Maihle N.J.;
7A 1.8 kb alternative transcript from the
factor receptor gene encodes a truncated
Nucleic Acids Res. 24:4050-4056(1996).
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              VGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCAR
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                                                                                                                                                                                         ASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTP 128
                                                                 KHSDCLACLHENHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTD
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                                         RESDCLVCRKFRDEATCKDTCPPLMLYNPTTYQMDVNPEGKYSFGATCVKKCPRNYVVTD
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E; PS00190; C)
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Eley G.D.;
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P.J., Yee D., Lau
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EMBL; AF27536; AAG28046.1; JOINED.
EMBL; AF275365; AAG28046.1; JOINED.
EMBL; AF275365; AAG28046.1; JOINED.
MGD; MGI:95294; Egfr.
InterPro; IPR000345; Cytc_heme_bind.
InterPro; IPR000345; EGFR_L.
InterPro; IPR000494; EGFR_L.
InterPro; IPR0002174; Furin-like.
pfam; PF00757; Furin-like.
pfam; PF01030; Recept_domain; 2.
SMART; SM00261; FU; 4.
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01-MAR-2001
01-JUN-2001
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Q9WVF5;
Q9WVF5;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mouse alternative
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                                                                                 VVTDHGSCVRACGPDYYEV-
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                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           FU; 4.
0; CYTOCHROME_C; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                       34.5%;
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16, Last
17, Last
RECEPTOR
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  12,
                                                                                 -EEDGIRKCKKCDGPCRK
                                                                                                                                                                                                                                                                                                                                                                                                                     MW;
                                                                                                                                                                                                                                                                                                                                                              43;
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                                                                                                                                                                                                                                                                                                                                                                        Score 789; DB 11;
Pred. No. 1.9e-60;
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Sciurognathi; Muridae;
                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                     DEF22002C84911B1 CRC64;
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S ISOFORM 2.
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jon T.R.,
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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kondo S., Yamanaka I.,
RA Arakawa T., Grawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kawai K., Okido T., Furuno M., Jamaida M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Lyons P., Marchionni L., Mashima J., Mazazarelli J., Mombaerts P.,
RA Lyons P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Haysehizaki Y.
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STRAIN-C57BL/6J; TISSUE-LIVER;
Reiter J.L., Threadgill D.W., Danielsen A.J., Schell
Lampland A.L., Balasubramaniam S., Crossley T.O., Mag
Maihle N.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-C3H/101, 129/SVJ, AND 129/SVEVTAC;
STRAIN-C3H/101, Threadgill D.W., Eley G.D., Strunk K.E., Danielsen ,
Reiter J.L., Threadgill R.S., Green P.J., Yee D., Lampland A.L.,
Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Alternative Transcripts from the Human and Mouse Carboxy-Terminal Truncated Receptors."; Submitted (JAN-1999) to the EMBL/GenBank/DDBJ data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheri
NCBI_TaxID=10090;
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                                                 Pfam;
Pfam;
                                                                                                                                EMBL;
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Hayashizaki Y.;
"Functional annotation of a full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21085660;
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EMBL; AF124513; AAD44149
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BL; ART275366; AAG28047.1;
BL; ARE775366; AAG28047.1;
BL; ARC975365; AAG28047.1;
BL; ARC04944; BAB23688.1;
BL; AK004944; BAB23664.1;
BL; AK004911; BAB23662.1;
D; MGI:95294; Egfr.
                                               PF00757;
PF01030;
                                  SM00261;
                                               IPR000494; EGFR_L.
    IPR002174; Furin-like.
10757; Furin-like; 1.
1030; Recep_L_domain; 2
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AA;
                                  FU;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mic sequence analysis and Egfr transcripts and
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Rodentia;
   72906
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Sciurognathi; Muridae;
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annotation update)
(EPIDERMAL GROWTH
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; Murinae; Mus
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Query Match
Best Local Similarity
Matches 156; Conser

Conservative

43;

Mismatches No.

116;

Indels

22;

Gaps

6,

34 46

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Score 789; DB 1 Pred. No. 2e-60;

DB 11;

Length

655;

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RESULT
Q9EP98
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Submitted (JUN-2000) t
EMBL; AF275366; AAG280
EMBL; AF275364; AAG280
EMBL; AF275365; AAG280
EMBL; AF275367; AAG240
EMBL; AF275367; AAG240
EMBL; AF275367; AAG240
                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=C57BL/6J;
Reiter J.L., Threadgi
Schehl C., Pearsall F
Balasubramaniam S., C
                                                                                                                                                                                                                                                                                                                                                                                                                      Q9EP98;
Q9EP98;
01-MAR-2001
01-MAR-2001
01-JUN-2001
EPIDERMAL GR
                                               InterPro;
InterPro;
InterPro;
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InterPro;
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Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen Sinclair C.S., Pearsall R.S., Green P.J., Yee D., Lampland A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D.,
                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                     mouse alternative
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"Comparative
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L GROWTH FACTOR F
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AAG28045.1;
AAG24386.1;
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Egfr transcr
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; Murinae; Mus
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PRESIDENT PRESID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9QX70 FACTOR Q9QX70;
Q9QX70;
f 01-MAY-2000 (TrEMBLrel. 13, Createu, 77 01-MAY-2001 (TrEMBLrel. 17, Last seq 77 01-JUN-2001 (TrEMBLrel. 17, Last and 77 101-JUN-2001 (TREMBLREL. 17, Last and 77 101-JUN-2001 (TREMBLREL. 17, Last and 77 101-JUN-2001 (TREMBLREL. 17, Last and 77 101-JUN-2001)
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Best I
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SMART; SM00220; S_TKC; 1.

SMART; SM00219; TyrKC; 1.

SMART; SM00219; TyrKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1

ATP-binding; Receptor; Transferase.

SEQUENCE 1210 AA; 134841 MW; 62CD02
                                                                                                                                           SEQUENCE FROM N
STRAIN=FISHER;
Petch L.A.;
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=FISHER; TISSUE=LIVER;
MEDLINE=90258888; PubMed=2342466;
MEDLINE=90258888; PubMed=2342466;
SEQUENCE FROM N.A.
STRAIN-FISHER; TISSUE-LIVER;
GUTTRIDGE K., Dawson T.L., E
Submitted (NOV-1999) to the
EMBL; M37394; AAF14008.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01030; Re PRINTS; PR00109;
                                                                                                                            Submitted
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Local Similarity
                                                                                                                                                                                                                             truncated, secreted form of the e coded by an alternatively spliced 1. Cell. Biol. 10:2973-2982(1990).
                                                                                                                                                                                                                                                                                              H.S
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                                                                                                                          (NOV-1991)
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                                                 N.A.
;; TISSUE=LIVER;
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; TISSUE=LIVER;
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9; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata;
Rodentia;
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                                           Earp
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                       EMBL/GenBank/DDBJ
                                                                                                                          EMBL/GenBank/DDBJ
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Pred. No. 4e-6
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Sciurognathi; Muridae;
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No. 4e-60;
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; Murinae; Rat
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RESULT 0922N7
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Q9Z2N7
Q9Z2N7;
Q1-MAY-1999 (TrEMBLrel. 10, Cr
T 01-MAY-1999 (TrEMBLrel. 10, Lr
JT 01-JUN-2001 (TrEMBLrel. 17, L
PROEPTOR TYROSINE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPRO00494; EGFR_L.

R InterPro; IPRO002174; Furin-like.

R InterPro; IPRO02174; Furin-like.

R InterPro; IPRO01245; Tyr_kin.

R InterPro; IPRO01245; Tyr_kin.

R Pfam; PF00757; Furin-like; 1.

R Pfam; PF000569; pkinase; 1.

Pfam; PF000069; pkinase; 1.

R Pfam; PF00009; TYRKINASE.

SMART; SM00109; TYRKINASE.

SMART; SM00219; TYRC; 1.

R PROSITE; PS00107; PROTEIN_KINASE_TOM; 1.

PROSITE; PS001107; PROTEIN_KINASE_TOM; 1.

PROSITE; PS00119; PROTEIN_KINASE_TOM; 1.

R PROSITE; PS00109; PROTEIN_KINASE_TOM; 1.

SMART-binding; Receptor; Transferase; Tyrosine-protein kinase.

SEQUENCE 1209 AA; 134890 MW; 96FEE7F6CC1B7773 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 157
                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; (Mammalia; Eutheria; )
NCBI_TaxID=10116;
[1]
                        InterPro;
InterPro;
InterPro;
InterPro;
                                                                                                                                         SEQUENCE FROM N.A.
TISSUE-HEART;
Zhao Y.Y., Kelly R.A., Smith T.W.;
Submitted (JAN-1998) to the EMBL/GE
EMBL; AF041838; AAD08899.1; -.
HSSP; P06213; 1IRK.
                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus
                                                                                                                        InterPro;
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157; Conserv
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                   ; IPRO00494; EGFR_L.
; IPRO00719; Euk_pkinase.
; IPRO02174; Furin-like.
; IPRO01368; TNFR_C6.
; IPRO01245; Tyr_kin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----YGTNKTGLRELPMRNLQEILIGAVRFSNNPILCNMETIQWRDIV-QDVFLSN
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                                                                                                                                                                                                                                                                                                                                       Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -GALEEKKVCQGTSNRLTQLGTFEDHFLSLQRMFNNCEVVLGNLE
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Last
                                                                                                                                                                                          EMBL/GenBank/DDBJ
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Pred. No. 1.8e-59;
4; Mismatches 117
                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence update)
annotation update)
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                                                                                                                   TISSUE-GASTRO-DUODENAL MUCOUS;
YU Y, Moshier J.A., Majumdar A.P.N.;
"Cloning of a novel EGFR-related peptid
regulator of EGFR.";
Submitted (SEP-1999) to the EMBL/GenBan
EMBL; AF187818 AAG17037.1;
InterPro; IPR000494; EGFR_L.
InterPro; IPR002174; Furin-like.
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O9ESEO;
O1-MAR-2001 (Trem
O1-MAR-2001 (Trem
O1-JUN-2001 (Trem
Receptor.
SEQUENCE
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prINTS; pR00109; TYRKINASE.
SMART; SM00261; FU; 4

SMART; SM00219; TYRKC: 1.

PROSITE; pS00107; pROTEIN_KINASE_ATP; 1.

PROSITE; pS00109; pROTEIN_KINASE_TYR; 1.
                                                                              Pfam;
                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Rode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ERRP.
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                                                                                                      Pfam;
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                     SM00261;
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     473
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(Tremblrel 16, Last seq
(Tremblrel 17, Last ann
(ROWTH FACTOR RECEPTOR REL
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                                                     FU;
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     52903
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Pred. No. 2.9e-59;
15; Mismatches 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
     4E0D7C3074F28973
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thi; Muridae;
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     CRC64;
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Matches 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIMILAR TO V-ERB-B2 AVIAN ERYTHROBLASTIC LEUKEMIA VIRAL
HOMOLOG 3.
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Q9BUD7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (FEB-2001) to the EMBL/GenBank/DDBJ EMBL; BC002706; AAH02706.1; -. 45B8EBEE683FE71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-CHORIOCARCINOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
    238
                                              247
                                                                                             179
                                                                                                                                     188
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nes 147; Conserv
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                                                                                                                                                                                                                                                                      GLLLALLPPGAA--STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCAR 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLLALLPPGAA--STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTN
PKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLST
                                                                                      NASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTT 127
                                                                                                                                                                                                                                                                                                                                                            GLLFSLARGSEVGNSQAVCPGTLNGLSVTGDAENQYQTLYKLYERCEVVMGNLEIVLTGH
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                                                                                                                                                                                 ----NSSHALRQLRLTQLTEILSGGVYIEKNDKLCHMDTIDWRDIVRDRD---AEIVVKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 734; DB 4;
Pred. No. 5.6e-56;
9; Mismatches 120;
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3; Mismatches
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Best Local
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SEQUENCE
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
RECEPTOR TYROSINE KINASE ERBB2 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                        Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctola
                                                                                                                                                                                                                                                            Relenisch T., Wolf P., Hombach-Klonisch S., Vogt S., Kuec Tetens F., Fischer B.; "ErbB genes and epidermal growth factor- (EGF-) like lice peri-implantation rabbit uterus and blastocyst."; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF333178; AAK14371.1; -.
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                                              TICAGGCARCKGOLPTDCCHEQCAAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTD 120
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Pred. No. 2e-55;
8; Mismatches 2
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Search completed: Job time: 325 sec April 11, 2002, 09:35:08

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Result
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000 Comp
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     US-09-146-283-4
US-08-579-823A-4
US-08-444-195-4
US-08-4467-083-68
US-08-4467-417B-68
US-08-484-438-68
US-08-466-545B-68
US-08-466-545B-68
US-08-466-5680B-68
US-08-466-680B-68
US-08-484-438-7
US-08-484-438-10
US-08-484-438-2
US-08-484-438-2
US-08-484-438-3
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Sequence 4, Appli Sequence 4, Appli Sequence 68, Appli Sequence 7, Appli Sequence 7, Appli Sequence 10, Appli Sequence 10, Appli Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 2, Appli Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli
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	1367 1367 383 383 1724 376 370 379 1940 799 799 799 799 881 881 881 915 288	
	23344444422	
ALIGNMENTS	US-08-625-819-2 US-08-746-559A-2 US-08-746-559A-5 US-08-857-076-105 US-08-857-076-12 US-08-857-076-103 US-08-857-076-104 US-08-857-076-106 US-08-857-076-106 US-08-644-271-30 US-08-525-940-23 US-08-525-940-21 US-08-525-940-21 US-08-525-940-21 US-08-525-940-21 US-08-525-940-21 US-08-525-940-21 US-08-525-940-18 US-08-525-940-18 US-08-525-940-18 US-08-525-940-18 US-08-525-940-18 US-08-525-940-18 US-08-525-940-18	
	Sequence 2, Appli Sequence 2, Appli Sequence 5, Appli Sequence 105, Appl Sequence 104, Appl Sequence 104, Appl Sequence 106, Appl Sequence 200, Appl Sequence 21, Appl Sequence 11, Appl Sequence 18, Appl Sequence 18, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl	

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; ORGANISM: homo sapiens ; INDIVIDUAL ISOLATE: GM-CSF-Her-2 fusion protein; Fig. US-09-146-283-4
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US-09-146-283-4
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                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Judge, Linda R.
REGISTRATION NUMBER: 42,702
REFERENCE/DOCKET NUMBER: 7636
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                            TELEFAX: 650-324-0960 INFORMATION FOR SEQ ID NO: 4:
                                                                TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 782 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ruegg, Curtis L.
APPLICANT: Wu, Hongyu
TITLE OF INVENTION: Immunostimulatory Compositions
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Deblinger & Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Laus, Reiner
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CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09, FILING DATE: 03-SEPT-1998 CLASSIFICATION: 536
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Matches 362;

Conservative

Query Match Best Local Similarity

82.1%; 83.0%;

Score 1878; Pred. No. 5.

DB 2; .1e-156;

Length 782; Indels 2

20;

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Mismatches

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US-08-579-823A-4
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                                                                                                   APPLICATION NUMBER: US/08/579,823A FILING DATE: 03-DEC-1998 CLASSIFICATION: 536 ATTORNEY/AGENT INFORMATION: NAME: Judge, Linda R. REGISTRATION NUMBER: 7636-0010 REFERENCE/DOCKET NUMBER: 7636-0010 TELECOMMUNICATION INFORMATION: TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                       TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 4:
            TYPE: amino acids
TOPOLOGY: line

OLECHTON

TOURS: line

OLECHTON
                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Laus, Reine APPLICANT: Ruegg, Curt APPLICANT: Wu, Hongyu
                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
MOLECULE TYPE:
HYPOTHETICAL:
                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                STREET: 350 Camb
CITY: Palo Alto
STATE: CA
COUNTRY: USA
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350 Cambridge Ave. Suite
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protein
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; ORGANISM: homo sapi
; INDIVIDUAL ISOLATE:
US-08-579-823A-4
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Patent No. 6210662
GENERAL INFORMATION:
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Best Local Similarity
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APPLICATION NUMBER: US/09/344,195
FILING DATE: 24-Jun-1999
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/146,283
FILING DATE: 03-SEPT-1998
                                                                                                                   COUNTRY: USA
ZIF: 94306
ZIF: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                         SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger &
                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Immunostimulatory Compositions NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                  Wu, Hongyu
                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                            STATE: CA
                                                                                                                                                                                                                           CITY: Palo Alto
                                                                                                                                                                                                                                         STREET:
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Ave. Suite
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Best Local S
Matches 362
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Patent No. 5726023
GENERAL INFORMATION:
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                                     APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES
TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
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             STREET:
                              ADDRESSEE:
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REGISTRATION NUMBER: 42,702
REFERENCE/DOCKET NUMBER: 76:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: homo sapiens
INDIVIDUAL ISOLATE: GM-CSF-Her-2 fusion
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 782 amino acids
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                                                                                                                                                                                                                                                                                                                                               IQEFAGCKKIFGSLAFLPESFDGDPASNT---APLQPEQLQVFETLEEITGYLYISAWPD
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Similarity 83.0%;
62; Conservative
Seattle
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            6300 Columbia Center, 701 Fifth Avenue
                                Seed and Berry
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Pred. No. 5.1e-156;
9; Mismatches 45;
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FILING DARF: 06-JUN-1995
ATTORNAY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 92001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
TELEEX: 3723836 SEEDAMBERRY
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
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APPLICATION NUMBER: US/00
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US
ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
                                                                                                                                                                                 AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
                                                                                                                                                                                                                                              LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
                                                                                                                                                                                                                                                                                                         DPLNNTTPYTGASPGGLRELQLRSLTEILKGGYLIQRNPQLCYQDTILMKDIFHKNNQLA 180
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                              --PDAHVAVNLSRYEG
                                                                                         LRMQPG--PAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPI-----SPVSVGRGPD 405
                                                                                                                       YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSAN 360
                                                                                                                                    YNYLSTDVGSCTLVCPLHNQEVTAEDGTQRCEKCSKPCAR-----GTHSLLPRPAAVPVP 355
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                                                              IQEFAGCKKIFGSLAFLPESFDGDPASNT---
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83.0%;
                               419
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                                                           -APLQPEQLQVFETLEEITGYLYISAWPD
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RESULT 5
US-08-414-417B-68
; Sequence 68, Application U
; Patent No. 5801005
; Patent No. 5801005
; GENERAL INFORMATION:

US/08414417B

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Best Local Similarity
Matches 362; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Sharkey, Richard G.
REGISTON NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/00
FILING DATE: 31-MAR-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION: IMMUN
TITLE OF INVENTION: FOR D
TITLE OF INVENTION: HER-2
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                                                                                                                                                             YNYLSTDYGSCTLYCPLHNQEVTAEDGTQRCEKCSKPCAR-----GTHSLLPRPAAVPVP 355
                                                                                                                                                                                                                                                                         AAGCTGPKHSDCLACLHFNHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACP 300
                                                                                                                                                                                                                                                                                                                                                            LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
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                                   --PDAHVAVNLSRYEG 419
                                                                                                                                                                                                                                                                                                                                                                                                                     DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
SLPDLSVFQNLQVIRG 433
                                                                            | TQEFAGCKKIFGSLAFLPESFDGDPASNT---APLQPEQLQVFETLEEITGYLYISAWPD
                                                                                                                        LRMQPG--PAHPVLSFLRPSWDLVSAFYSLPLAPLSPTSVPI-----SPVSVGRGPD 405
                                                                                                                                                                                                                                                                                                                                    LTLIDTNRSRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQC 240
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83.0%; Pred. No. 9.5e-156;
vative 9; Mismatches 45;
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FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
HER-2/neu ONCOGENE IS ASSOCIATED
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Best Local Similarity
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Patent No. 5811098 5780031
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                                                                                                                                                                                                                           Matches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/323,442
FILING DATE: 14-OCT-1994
APPLICATION NUMBER: US 08/150,704
FILING DATE: 10-NOV-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: unka
TOPOLOGY: unknown
MOLECULE TYPE: prot
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APPLICANT:
APPLICANT:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/981,165
FILING DATE: 24-NOV-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Missook & Tocio
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COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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                   121 DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
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OPERATING SYSTEM:
SOFTWARE: Patentl
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REGISTRATION NUMBER: 18,8
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                                                                                                                                               1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
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DPLNNTTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLA 180
                                                                       ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
                                                                                         ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNG 120
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Hellstr m, Karl E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PE: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Pred. No. 9.5e-156;
9; Mismatches 45;
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                                                                                            Matches 362;
                                                                                                          Best Local Similarity
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                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-631
INFORMATION FOR SEQ ID NO: 68:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,348A
FILING DATE: 07-JUN-1995
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TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
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   61
                                                                                                                                                                                  TYPE: amino acid TOPOLOGY: linear
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                                               1 MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL 60
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                              MELAALCRWGLLLALLPPGAASTQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNL
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                                                                                            Conservative
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83.0%;
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                                                                                         Score 1878; DB 2;
Pred. No. 9.5e-156;
9; Mismatches 45;
                                                                                                                    Length 1255;
                                                                                          Indels
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                                                                                                                       TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 2:
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                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
                                                                                                                                                             REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible .
COMPUTER: PC COMPATIBLE .

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: REACTIVITY TO HER-2/neu PROTEIN FOR PREVENTION
TITLE OF INVENTION: OR TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu
TITLE OF INVENTION: ONCOGENE IS ASSOCIATED
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APPLICANT: Disis, Mary L.
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                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/01
FILING DATE: 01-APR-1996
CLASSIFICATION: 424
                                            TOPOLOGY:
                                                                 TYPE:
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NO. 5869445
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RESULT 9
US-08-468-545B-68
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                    TELEFAX: (206) 682-603 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                   NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920
TELECOMMUNICATION INFORMATION:
                                                                                                                                        CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G
                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
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CITY: S
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                                                                     TELEPHONE:
                                                                                                                                                                                      APPLICATION NUMBER: US/01 FILING DATE: 06-JUN-1995
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GENERAL INFORMATION:
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Best Local :
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APPLICANT:
APPLICANT:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/831,967
FILING DATE: 06-FEB-1992
                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Edmund R. Pi.
STREET: Exchange Place,
                                                                                                                                                                                                                                                                                                                    APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosyr
TITLE OF INVENTION: Market
NUMBER OF SEQUENCES: 16
                                                                                   CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                     STATE: Mass
COUNTRY: US
ZIP: 02109
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                                                                    FILING DATE
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les 362; Conserv
                                                                                                                       SOFTWARE:
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GY: linear
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                                                                                                                                                                                                                                       Massachusetts
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Oppermann, Hermann
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                                                                                                                     PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                     Biosynthetic Binding Protein
Marker
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83.0%;
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                                                                                      US/08/356,786
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ce, 53 State Street
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Pred. No. 9.5e-156;
9: Mismatches 45;
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; Sequence 68, Application US/08466680B
; Patent No. 6075122
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Best Local Similarity
                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                 APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH
TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: .1255 amino acids
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NAME: Pitcher, Edmund R.
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                                 COUNTRY: US
ZIP: 98104-7092
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                                                                STATE:
                                                                                                             ADDRESSEE:
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                                                                                                           Seed and Berry LLP
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83.0%;
                                                                                            Center,
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Pred. No. 9.5e-156;
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                                                                                            701 Fifth Avenue
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Sequence 1, Application US/08422108
Patent NO. 6015567
GENERAL INFORMATION:
APPLICANT: Hudziak, Robert M.
APPLICANT: Shepard, H. Michael
APPLICANT: Ullrich, Axel
TITLE OF INVENTION: HER2 EXTRAC
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US-08-422-108-1
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INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
                                                CORRESPONDENCE ADDRESS
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                    NUMBER OF SEQUENCES:
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ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
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                                                                                                                                                                                       Application US/08422108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1255 amino acids
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                                                                                  HER2 EXTRACELLULAR
                                                                                                                   H. Michael
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                                                                                    DOMAIN
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy

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RESULT 13
US-08-336-708A-9
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FILING DATE: 13-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/048
FILING DATE: 15-APR-1993
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ATTORNEY/AGENT INFORMATION:
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LASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                              61 GYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTPVTGASPGGLRELQ
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les 341; Conserv
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                                                                                                       DLVSAFYSLPLAPLSPTSVPI-----SPVSVGRGPD--PDAHVAVNLSRYEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTNASLSFLQDIQEVQ 81
                                                                                                                                                   VTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTSANIQEFAGCKKIFGSLAFLPESF
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                                                   US-08-484-438-7
                                                                       RESULT
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Sequence 7, Application US/08484438 Patent No. 5811098 Patent No. 5811098 5780031
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Best Local Similarity 45.3
Matches 151; Conservative
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APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER:
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CITY: Thousand Oaks
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                                                                                                                           HGSCVRACGADSYEM-EEDGVRKCKKCEGPCRK 335
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1840 Dehavilland Drive
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Chang, Ming-Shi
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GENERAL INFORMATION:

APPLICANT:

Plowman, Gregory D. Culouscou, Jean-Michel

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US-08-484-438-7
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Best Local (
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APPLICANT:
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REFERENCE/DOCKET NUMBER: 56
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/3
FILING DATE: 14-OCT-1994
APPLICATION NUMBER: US 0
FILING DATE: 10-NOV-1993
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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RESDCLVCRKFRDEATCKDTCPPLMLYNPTTYQMDVNPEGKYSFGATCVKKCPRNYVVTD
                                                             LGSCQKCDPSCPNGSCWGAGEENCQKLTKIICAQQCSGRCRGKSPSDCCHNQCAAGCTGP
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10036-2711
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Hellstr m, Karl E.
IVENTION: HER4 HUMAN RECEPTOR TYROSINE
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                                                                                                                                                                                                                                                                                                                                                   Matches 151;
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: HUMAN GENE RELATED TO BUT DISTINCT FROM TITLE OF INVENTION: EGF RECEPTOR GENE NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: KING,
APPLICANT: KRAUS,
APPLICANT: AARONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
 244
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FILING DATE: 7 Jun 1995
CLASSIFICATION: 435
                                                                                                                                                                                                           74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 14
                                                                                                                                                                                                                                                                                                  11 LLLALLPPGAA--STQVCTGTDMKLRLPASPETHLDMLRHLYQGCQVVQGNLELTYLPTN 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Perryman, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Atlanta
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                KHSDCLACLHFUHSGICELHCPALVTYNTDTFESMPNPEGRYTFGASCVTACPYNYLSTD 307
                                                                                                                                                          VTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQLALTLIDTNR 188
                                                                                                                                                                                                                            ASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTQLFEDNYALAVLDNGDPLNNTTP 128
                                                                                    SRACHPCSPMCKGSRCWGESSEDCQSLTRTVCAGGCA-RCKGPLPTDCCHEQCAAGCTGP 247
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RESDCLVCRKFRDEATCKDTCPPLMLYNPTTYQMDVNPEGKYSFGATCVKKCPRNYVVTD
                                                                   {\tt LGSCQKCDPSCPNGSCWGAGEENCQKLTKIICAQQCSGRCRGKSPSDCCHNQCAAGCTGP}
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7: USA
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Suite 1200, 127 Peachtree (
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                                                                                                                                                                                                                                                                                                                                                 34.7%; Score 793; DB 2;
45.3%; Pred. No. 6.7e-61;
tive 50; Mismatches 118
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